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Minimum
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Perfect score:
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length: 2000000000
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em_htg_pln:*
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REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 169620)
Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,

RESULT 1
AC012674/c
LOCUS
DEFINITION

AC012674 169620 bp Homo sapiens chromosome 3 clone 18 unordered pieces.

DNA RP1-458H3,

WORKING

DRAFT SEQUENCE, HTG

07-SEP-2000

ALIGNMENTS

ACCESSION VERSION

AC012674 AC012674.10 GI:9719580

HTGS_PHASE1; HTGS_DRAFT

SOURCE KEYWORDS

ORGANISM

Homo sapiens

Homo sapiens.

score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. printed,

SUMMARIES

Result o o C 000 000 Ω aα No Score 100 Match Query 000 38936 124271 110000 166706 207408 Length 169772 108040 1347 153940 DB AC012674 AL137847 U66060 AC016216 HS253J14 CNS01RHY AC022694 AC090811 AC022695 HSTCRBV AC023971 AC020717 HSDJ60101 AL365267 AC092375 AC025421 AC092285 AC068150 AC099484 AC019030 AC092119 AC015493 AC069538 AL607077 AL691517_2 AC068875 AC068618 AC068618 AP001019 AC034249 AC090762 AC007445 AL358817 AC025179 AC008814 AC121249 AC121249 AC107979 AC103996 AC104303 IJ AL591491 Ac021025 Homo sapi Ac076969 Homo sapi Ac121249 Homo sapi Ac107979 Homo sapi Ac103996 Homo sapi Ac103996 Homo sapi Ac090762 Homo sapi Ac090762 Homo sapi Ac007445 Homo sapi Ac358817 Human DNA AC068875 Homo sapi AC06818 Homo sapi AC087283 Homo sapi AC087294 Homo sapi AC079737 Homo sapi AC026324 Homo sapi AC026324 Homo sapi AC026324 Homo sapi AC09948 Homo sapi AC09948 Homo sapi AC019030 Homo sapi AC019030 Homo sapi AC015493 Homo sapi AC015493 Homo sapi AC015493 Homo sapi AL162633 Human chr AC022694 Homo sapi AC090811 Homo sapi AC022695 Homo sapi AC025179 AC008814 AP001019 AC034249 AL109656 AL365267 U03115 Hu AC012674 Homo AL137847 Humar Description AL607077 Human DNA Continuation (3 of U66060 Human germl AC016216 Homo sapi Z80771 Human DNA s AC069538 AC023971 Homo sapi AC020717 Homo sapi AC092285 67 Human DNA Human V bet Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Human DN2

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Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kongy, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M. Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Oswal, G., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shah, S., Weinstock, G., Weinstock, T.R., Williamson, A., Warlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 7, 2000 this sequence version replaced gi:8705345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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107262
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Consensus quality: 139025 bases at least Q40
Consensus quality: 154842 bases at least Q30
Consensus quality: 159725 bases at least Q20
Estimated insert size: 162720; sum-of-contigs estimation
Estimated insert size: 171608; agarose-fp estimation
Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.1x in Q20 bases; sum-of-contigs estimation
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Center clone name: RP1-458H3
Center clone Summary Statistics
                                                                126940
127040
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Contact: hgsc-help@bcm.tmc.edu
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                                                       gap of contig gap of contig gap of contig gap of contig
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contig
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JOURNAL

ERENCE AUTHORS TITLE

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VERSION
KEYWORDS
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AL137847/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTTGCAGGGACTTCTGGGGCCC 60
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw:
                                                                                                                                                                    Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 17, 2001 this sequence version replaced gi:16408610 on Nov 17, 2001 this sequence version replaced gi:16408610 ouring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        Kimberley, A.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence. AL137847
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/db_xref="taxon:9606"
/chromosome="3"
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length
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bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on chromosome 9q22.2-31.1,
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                                                                                                                                                                                         we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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WORMPEP;

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RESULT 3
AC021025/c
ID AC0210
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ORIGIN
RA BOUCK J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J.,
RA BOUCK J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J.,
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Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,
RA Ferraguto D., Forcum-Tansey J., Frantz P., Ganesh R., Gorrell J.H.,
RA Gorrell L.L., Guevara W., Harris K., Hernandez J., Hodgson A., Hogues M.,
RA Gorrell S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,
RA Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,
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RA Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,
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RA Martinez C., McLeod M.P., Mei G., Morgan M., Morriss S., Nash S., Nelson A.,
RA Martinez C., McLeod M.P., Mei G., Barish B., Paxton S., Payton B.,
Perez L., Pu L.L., Quiles M., Reiter D., Rives M., Samuel S., Say J.,
RA Scherer S., Shah E., Shah H., Simon M., Sparks A., Stamps A., Sucgang R.,
RA Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,
RA Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,
RA Watlington J., Wrensford G., Yu W., Zhou X., Nelson D., Gibbs R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome 3 clone RP11-79K17, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC021025.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC021025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_DRAFT; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC021025;
                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone RP11-439K3 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-39K3 is at 1 in this sequence true left end of clone RP11-344L17 is at 141373 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chr9
RP11-439K3 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp: Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42809
                                                                                                                                                                                                                                                                                                                                                                                                                 Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.2%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11.2"
30224 c 28152 g 42187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="q22.2-31.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .143372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; HTG; 123779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last updated, Version 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB; Pred. No. 9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Le..
.o. 9.6e-17;
.o. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                           Query Match
Best Local Similarity
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Matches

FEATURES

36.0%; 100.0%;

Score Pred.

40;

DB 30;

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Consensus quality: 112332 bases at least Q40 Consensus quality: 117272 bases at least Q30 Consensus quality: 119789 bases at least Q20 Consensus quality: 119789 bases at least Q20 Estimated insert size: 121963; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Direct Submission";
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye:
Assembly program: Phrap; version 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Aug 7, 2000 this sequence version replaced gi:8700003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JAN-2000) to the EMBL/GenBank/DDBJ databases. Human Genome Sequencing Center, Department of Molecular and Baylor College of Medicine, One Baylor Plaza, Houston, TX '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: HMXB
Center clone name: RP11-79K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley K.C.
Sequence
                                                                                                                             source
                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -123779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                 112908
113008
                                                                                                                                                                                                                                                                                                                                        96822
105595
105695
                                                                                                                                                                                                                                                                            120199
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36032
60755
60855
71668
71768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     code:
  123779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                        35931: contig of 35931 bp in le
36031: gap of unknown length
60054: gap of unknown length
71567: contig of 13059 bp in le
71767: gap of unknown length
84826: contig of 13059 bp in le
84926: gap of unknown length
96721: contig of 11795 bp in le
96821: gap of unknown length
105694: contig of 71795 bp in le
105694: gap of unknown length
112907: contig of 7213 bp in ler
113007: gap of unknown length
112907: contig of 7213 bp in ler
113007: gap of unknown length
120198: contig of 7191 bp in ler
120298: gap of unknown length
122220: contig of 1922 bp in ler
122220: contig of 1922 bp in ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCM
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BP; 37802 A;
                                                           /chromosome="3"
/db_xref="taxon:9606"
/organism="Homo sapiens"
                                                                                                                                                                 Location/Qualifiers
                                         /clone="RP11-79K17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Information
                                                                                                                                                                                                             unknown
of 1459
24017 C;
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23437 G; 37612 T; 911 other;
                                                                                                                                                                                                                                                      length
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KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION DEFINITION rocus В

Matches

40;

69

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3083 AAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCT 3044
                                                                                                                                                                                                                                                                                                                                                                 DukaryCtts: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 128118)

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bilmage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Bileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burchly,K.L., Byrd,N.C., Carron,T.F., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,R., L., Diny,Y., Dinh,H.H., Douthwaite,K.J., Drayds,C., Dany-Carroll,L., Dederich,D.A., Delaney,R.R., Delgado,O., Denn,A.L., Diny,Y., Dinh,H.H., Douthwaite,K.J., Drayds,C., Edecito,M., Falls,T., Ferraguto,D., Elagy,N., Eord,J., Elhal,C., Escotto,M., Falls,T., Ferraguto,D., Elagy,N., Eord,J., Elhal,C., Escotto,M., Falls,T., Ferraguto,D., Elagy,N., Eord,J., Elhal,C., Escotto,M., Falls,T., Ferraguto,D., Law,Y., Hamaldex,J., Harris,K., Hart,M., Havlak,P., Hawe,S., Hamilon,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawe,S., Hamilon,K., Harris,C., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,E., Yacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Kartsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,A., Mujas,E., L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louises,E., Massey,E., Mawhiney,E., Mcleod,M.P., Meador,M., Mers,E., Maysey,B., Miner,Z., Mitchell,T., Mohabbat,K., Morris,E., Maysey,B., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuconu,G., Oragunye,N., Notkerson,E., Nwokenkwo,S., Nulla,R., Mayse,B., Scherer,S., Scott,G., Shen,H., Shooshitari,N., Sison,H., Soherer,S., Sonatke,T., Sparks,A., Stanley,H., Sison,I., Soherer,S., Sonatke,T., Sparks,A., Stanley,H., Mallamson,A., Wleczyk,R., Mooden,S., Wallamson,R., Wallalmson,R., Wleczyk,R., Wooden,S., Weisson,D., Wallamson,R., Wleczyk,R., Wooden,S., Walland,R., Mayse,M., W., F., Zhou,J., Zorrill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCT
                                                                                                                                Baylor
On Oct
                                                                                                                                                     Submitted (01-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                            Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACO76969 128118 bp DNA linear HTG 15-OCT-2001 Homo sapiens chromosome 3 clone RP11-79K12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                           Oct 14, 2001 this sequence version replaced g1:10047573
                                                                                                                                                                                                                                                                                   (bases 1 to 128118)
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     Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
Homo sapiens chromosome
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	COMMENT	JOURNAL	REFERENCE AUTHORS	AUTHORS TITLE JOURNAL	TITLE JOURNAL	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
Center Code: Web. 1970/www.genome.washington.edu Contact: uwgchigsel.washington.edu Contact: uwgchigsel.washington.edu Drafting Center: BCM	On May 16, 2002 this sequence version replaced gi:9719675.	Direct Submission Submitted (01-JUN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA	3 (bases 1 to 128583) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D. Direct Submission Submitted (16-MAY-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA	and Haugen,E.D. Direct Submission Unpublished 2 (bases 1 to 128583)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 128583) Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.	AC121249 AC021025 AC121249.1 GI:20806313 HTG. human. Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. E 1 (bases 1 to 148290) S Birren, B., Nusbaum, C., and Lander, E. Homo sapiens chromosome 15, clone CTD-3049M7 L Unpublished E 2 (bases 1 to 148290) S Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, C., Congel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goytte, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamatt, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Liu, G., MacLean, C., McCarathy, M., MacCwan, P., Major, J., Maglarim, J., Manthews, C., McCarthy, M., McCwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Morbu, C., McCarthy, M., Malenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,	AC107979 Homo sapiens AC107979 AC107979.7 (HTG. HTG.	AAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCT	Query Match Best Local Similarity 100 Matches 40; Conservative	/d /c /c /c 37777 a				1321	4615	1890	26	1670	836	:	750	1137
Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 148290) Birren,B., Nusbaum,C. and Lann Homo sapiens chromosome 15, C. Unpublished 2 (bases 1 to 148290) Birren,B., Linton,L., Nusbaum, Anderson,S., Barna,N., Basties Brown,A., Comarata,J., Campop; Choepel,Y., Colangelo,M., Coll Cooke,P., DeArellano,K., Dewas Ferreira,P., FitzHugh,W., Gagg Ginde,S., Gord,S., Goyette,M., Kamat,A., Karatas,A., Kells,C. Landers,T., Lehorzky,J., Levir Macdonald,P., Major,J., Marqui McEwan,P., McKernan,K., Meldri McEwan,P., McKernan,K., Meldri McEwan,P., McKernan,K., Meldri	14 3 chromosome GI:21592043	CTCTGTGTGTGCC TCTGTGTGTGCC	0%; S .0%; 0;	/db_xref="taxon:9606" /chromosome="3" /chromosome="3" /clone="RP11-79K17" /clone=lib="RPCI human B. /clone_lib="RPCI human B. 24752 c 24789 g 4126	Location/Qualifiers 1128583			1273	4522	1872	2609		887		749	1065
ordata; Craniata; Vertebrata; Eutel imates; Catarrhini; Hominidae; Home and Lander, E. ne 15, clone CTD-3049M7 Nusbaum, C., Lander, E., Ali, A., Alle Bastien, V., Boguslavkiy, L., Boukhg Campopiano, A., Chang, J., Chazaro, B. M., Collins, S., Collymore, A., Cook, M., Collins, S., Collymore, A., Cook, M., Gale, D., Galagan, J., Gardyna, S., rette, M., Graham, L., Grand-Pierre, M., ulme, W., Iliev, I., Johnson, R., Jone Kells, C., LaRocque, K., Lamazares, R, Levine, R., Liu, G., MacLean, C., , Marquis, N., Matthews, C., McCarthy Meldrim, J., Meneus, L., Mihova, T., Naylor, J., Nguyen, C., Nicol, R., Nor	bp lone	TGAGTGGCTGCT TGAGTGGCTGCT	Score 40; DB 9; Pred. No. 4.3e-); Mismatches	1:9606" 1K17" 1K17 BAC 1 human BAC 19 g 41265 t	iers						7555		10	;	1	798
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inidae; Euteleost inidae; Homo. Allen,N. Allen,N. Allen,N. Boukhgalte y,L. Boukhgalte y,L. Boukhgalte gouldens son,R. Jones,C. Lamazares,R., acLean,C., McCarthy,M., Mihova,T.,	DNA linear PRI CTD-3049M7, complete s		Length 128583;	11"		i	367	4130	7	4185	1371			4438		1896
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Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 26, 2002 this sequence version replaced gi:21321840. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 148290)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barnà,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cooke,A., Cooke,P., DeArellano,K., Day, G., Garan G., Cooke, P., Dearellano,K., Diaz,J.S., Dodge,S.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L.,
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Direct Submission
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Center project name: L24533
Center clone name: 3049_M_7
                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                       Center code: WIBR Web site: http://w
                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT
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                                                                                                                                                                                                                                                                               http://www-seq.wi.mit.edu
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/rpt_family="MIR3"
11129. .11224
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6377. .6581
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/rpt_family="MIR"
               /rpt_family="AluSq"
complement(32582. .32777)
/rpt_family="".""
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/rpt_family="L2"
27917..28357
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/db_xref="taxon:9606"
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/rpt_family="L2"
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26293. .26417
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21635
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5727. 5766
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                                                                                       complement(31182. .31787)
/rpt_family="L2"
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29716. .29790
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RS Biren, B. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Biren, B., Linton, L. Nusbaum, C., Cangelavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Camppiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, E., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCean, S., Kanatas, A., Kells, C., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Maccarthy, M., McEwan, P., McKernan, Y., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Connell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillio, J., Vassiliev, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165649 bp DNA linear PRI 01-JUL-2
Homo sapiens chromosome 15, clone RPI1-76E17, complete sequence.
AC103996
AC103996.7 GI:21637504
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 15, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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36831.
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41414. .41616
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33877...34506
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5. .33500
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FEATURES SOURCE repeat repeat	TITLE URNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
RES Location/Qualifiers 1. 16549 /organism**Homo sapiens** /db_xref="taxon:9606* /chromosome="15" /map="15" /clone="RP11-76E17* /clone="RPCI-11 Human Male BAC" /clone=lib="RPCI-11 Human Male BAC" /clone=lib="RLI" /clone="RLI" /clone="RL	O'Connor, T., O'Donnell, P., O'Neil, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange Thomann, M., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 1, 2002 this sequence version replaced gi:21592191. All repeats were identified using RepeatMasker: Smit, A. F. A., & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission L. Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases I to 16549) B airren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Comarata, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gradyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Miccarthy, M., Meldrim, J., Meneus, N., Michova, T., Menga, V., Maccarthy, M., Meldrim, J., Meneus, N., Michova, T., Menga, V., Maccarthy, M., Meldrim, J., Meneus, N., Michova, T., Menga, V., Marchell, M., Marchell, M., Maccarthy, M., Meldrim, J., Meneus, N., Michova, T., Meneus, N., Michova, T., Meneus, N., Michova, T., Maccarthy, M., Meldrim, J., Meneus, N., Michova, T., Meneus, N., Michova, T., Meneus, N., Michova, T., Michova,	Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 165649) Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkly, L., Boukbgalter, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
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/rpt_family="L2" 20049 . 20114 /note="single clone coverage" 20485 . 20655 20485 . 20655 complement(21285 . 21441) /rpt_family="MIR3" /rpt_family="MIR" 21496 . 21717 /rpt_family="L2" complement(21720 . 21796) /rpt_family="MIR"	TPET ramily="LING3" COMPLEMENTY 521816449) COMPLEMENTY 521816449) COMPLEMENTY 521816449) COMPLEMENTY 521816449 COM	/rpt_family="LIM4c" complement(44614755) /rpt_family="Alusx" 50275397 /rpt_family="L2" complement(56506330) /rpt_family="LIME1" complement(65696460) /rpt_family="LIME1" 72147319 /rpt_family="LIMC3" 73547655 /rpt_family="LIMC3" 73547655 /rpt_family="LIMC3" 77557743 /rpt_family="LIMC3" 76597743 /rpt_family="LIMC3" 784414156 /rpt_family="LIMC3" 784414156 /rpt_family="LIMC3"	/rpt_family="L1PA13" complement(8951248) /rpt_family="THENA" complement(12491504) rpt_family="L1PA13" 15051659 /rpt_family="CAAA)n" 16271659 /rpt_family="(CAAA)n" 16601831 rpt_family="AluSx" complement(18323132) /rpt_family="L1PA13" complement(18103699)

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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-FEB-2002) Genome Center, University of Washington, Box 353145, Seattle, WA 98195, USA
On Feb 25, 2002 this sequence version replaced gi:17402782.

Center: University of Washington Genome Center Center Code: UNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 178650)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 178650)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
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Kaul, R.K., Olson, M.V., Zhou, Y.,
Saenphimmachak, C., Phelps, K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                          Sequencing vector: unknown; 55% of reads Sequencing vector: plasmid; 45% of reads Chemistry: Dye-terminator ET; 89% of reads Chemistry: Dye-terminator Big Dye; 11% of reads
                                                                                                                                                  Center project name: chr-3
Center clone name: RP11-391P4 (bc0402)
                                                                                                                                                                                                                                                                                    Drafting Center: WUGSC
                                                                                                                                                                                                                                                                                                           Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                Web site: http://www.genome.washington.edu
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/rpt_family="MIR"
23082 .23195
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/rpt_family="MLTIA2"
26142...26334
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/rpt_family="MIR"
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/rpt_family="MIR"
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/rpt_family="MIR"
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program: Phrap;
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                                                                                                                                                                                                                                                      Project Information
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      version 0.990319
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. 4.3e-12;
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Consensus quality: 178494 bases at least consensus quality: 178631 bases at least consensus quality: 178650 bases at least insert size: 178648; sum-of-contigs
Quality coverage:
8.0x in Q20 bases; sum-of-contigs
                                              030
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Overlapping Sequences: 5': RP11-475023 (UWGC:bc0439) AC023346 RP11-79K12 AC076969

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phre quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Phred

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies in the table. There are no significant remaining discrepancies of the sequence of the sequence

<800	361	2683	2	783	743
1541	1550	<800	321	2923	3045
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Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,	JOURNAL Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA REFERENCE 3 (bases 1 to 192826) AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,	Soughez,C., Spencer,B., Stange-Thomann,N., StoJanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.	Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Rise, C., Rogov, P., Rogov	Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzHugh, W., Gadge, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,	Homo sapiens chromosome 15, clone RPII Unpublished 2 (bases 1 to 192826) Birren, B., Linton, L., Nusbaum, C., Lande Barna, N., Bastlen, V., Boguslavkiy, L., I Camarata, J., Campopiano, A., Choepel, Y.	SE SM	RESULT 9 AC090762/c AC090762 192826 bp DNA linear PRI 28-FEB-2002 DEFINITION Homo sapiens chromosome 15, clone RP11-387E8, complete sequence. ACCESSION AC090762 VERSION AC090762.9 GI:18997378 KETWOORDS HTG.	Query Match 36.0%; Score 40; DB 9; Length 178650; Best Local Similarity 100.0%; Pred. No. 4.3e-12; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 69 AAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTT 108	1713 167 1713 280 1715 <80 1715 109 1717 1119 118

repeat_region complement(8117. 8452) /pt_family="AluJo" repeat_region 8540. 8639 /pt_family="MER45" repeat_region complement(8832. 8916) /pt_family="L2" repeat_region 10391. 10599 /rpt_family="MER3" repeat_region 11688. 11828 /pt_family="LIMC/D" repeat_region 12039. 12078 /rpt_family="AT_rich" repeat_region 12032. 12447 /rpt_family="THEIC"	/Organism="Homo Sapiens" /db_xref="htaxon:3606" /chromosome="15" /chromosome="15" /clone="htaxon:3606" /clone="htaxon:3606" /clone="htaxon:3606" /clone="htaxon:38788" /rpt_family="htlp3" repeat_region /rpt_family="htlp3" repeat_region /rpt_family="htlp3" repeat_region /rpt_family="htlp3" /rpt_family="	Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Romann, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Myman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission Submitted (28 FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2002 this sequence version replaced gi:18377189. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center whitehead Institute/ MIT Center for Genome Research Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project name: 112392 Center clone name: 387_E_8 FEATURES Location/Qualifiers FEATURES Source Location/Gualifiers FEATURES Feature Sequence Sequen
	repeat_region	repeat_region
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Lilton, E., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Worris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Conmor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-APR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 30, 2000 this sequence version replaced gi:8705092. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammatra, Warner 1 (bases 1 to 32918)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Birren, B., Cinton Chromosome 18, Clone RP11-344B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC007445 32918 bp DNA linear Homo sapiens chromosome 18 clone RP11-344B7 map 18, IN PROGRESS ***, 1 ordered piece.
                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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by the finished sequence as soon as it is available and the accession number will be preserved.
                                                provided by the submittor.
This sequence will be replaced
                                                                                               of the gaps
                                                                                                                                    consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces \alpha
                                                                                               is believed to be correct as given, he of the gaps between them are based on
                                                                                                                                                                                       NOTE: This is a 'working draft' sequence.
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                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                      Center clone name: 344_B_7
                                                                                                                                                                                                                                                            Center project name:
                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/
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*** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL358817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lovell, J.
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GGAGTATGTAAAACTCCTGGGTCTCTGTGTGTGTGCCTGAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                               sections only once, except for a short overlap.

The true left end of clone RP11-432J9 is at 36937 in this sequence.
                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/HGP/Chr10
RP11-399N22 is from the library RPCI-11.2 constructed
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the sanger Centre Chromosome 10
                                                                                                                                           RP11-399N22 It may be shorter because we sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
On Oct 9, 2001 this sequence version replaced g1:14669268.
                                                                                                                                                                                                        http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                             Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence AL358817
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                                                  true left end of clone RP11-432J9 is at 36937 in this sequence true right end of clone RP11-91A1 is at 2000 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 38936)
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Location/Qualifiers
1. .38936
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6493 c 6865 g
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                                                                                                                                                                        This sequence is not the entire insert of clone
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/db_xref="taxon:9606"
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Pred. No.
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1.6e-11;
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                                                                                                                                                                                            Consensus quality: 116609 bases at least Q40
Consensus quality: 120226 bases at least Q30
Consensus quality: 121274 bases at least Q20
Estimated insert size: 121276; agarose-fp estimation
Estimated insert size: 1217160; agarose-fp estimation
Quality coverage: 6.46 in Q20 bases; agarose-fp estimation
Quality coverage: 6.12 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary, Gaps between the contigs are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:7711794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Homo sapiens chromosome 5 clone
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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AC025179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Code: JGI
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DOE Joint Genome Institute.
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r: Joint Genome Institute
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9079 c 9111 g 11431 t
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/clone="RP11-399N22"
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/db_xref="taxon:9606"
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1052: contig of 1052 bp in length
1152: gap of unknown length
3331: contig of 2179 bp in length
3431: gap of unknown length
7470: contig of 3939 bp in length
7470: gap of unknown length
15483: contig of 8013 bp in length
15583: gap of unknown length
24916: contig of 9333 bp in length
      15483:
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Pred. No.
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CTD-2174B5,
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1.6e-11;
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DRAFT SEQUENCE,
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                61 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGTGCCTGAGT 99
                                                              l Similarity
39; Conser
                                                                                                                                                                                                                                                                        Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.3% of Sequence;
                                                                                                                                                                                                                                                                                                                                     Submitted (31-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Oct 31, 2001 this sequence version replaced gi:15290309. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 146671) DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-AUG-1999) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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Mammalia; Eutheria; Primates; C
1 (bases 1 to 146671)
DOE Joint Genome Institute and
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/chromosome="5"
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39922: contig of 14906 bp in 1
40022: gap of unknown length
68684: contig of 28662 bp in 1
68784: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-Jan-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Eax:81-42-778-9924)
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2 (bases 1 to 159747)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 159747)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 159,747 genomic DNA of 18pll.3
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Center project name: HumDraft18
Center clone name: RP11-752I11
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Contact: hattori@gsc.riken.go.jp
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Center code: RIKEN
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sapiens DNA, clone:RP11-752111
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148941 151243 contig of 2303 bp in length
15344 153454 contig of 2311 bp in length
153555 156134 contig of 2580 bp in length
156235 158089 contig of 1855 bp in length
158190 159747 contig of 1856 bp
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103976: contig of 7679 b

103977 104076: gap of 100 bp

104077 110726: contig of 6677

110727 110726: contig of 6677
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87874 87973: gap of 78235 87874 87973: gap of 7723
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18545 29631: contig of 11087 bp in length
                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/map="18p11.3"
/note="assembly_fragment"
                                                                                              clone="RP11-752I11"
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151243: cont
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8940
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145855: cont
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96197: contig of 8224 bp
97: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143: gap of 100 bp
57170: contig of 13927 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of 100 39: contig of 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
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econtig of 3598 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of 100 bp: contig of 2961 bp: 100 bp: 100 bp: contig of 2945 bp: contig of 2945 bp: 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ap of 100 bp
contig of 2580 bp
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contig of 3333 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ap of 100 bp contig of 2885 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 4776
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                 RESULT 15
AC034249
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ORIGIN
 REFERENCE
                                                                                                                                                                      ACCESSION
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Unpublished
2 (bases 1
                           1 (bases 1 to 162740)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                  Homo sapiens chromosome 5 clone RP11-427C17, WORKING DRAFT
                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                          Homo sapiens
                                                                                                                                         HTG;
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AC034249
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Similarity 100.0%;
39; Conservative
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158190. .159747
/note="assembly_fragment"
.30397 c 29897 g 49849 t
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/note="assembly_fragment"
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132719. .136051
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68341. .78134
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43244. .57170
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156235. .158089
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153555. .156134
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151344. .153454
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139850. .142810
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136152. .139749
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122890. .127665
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57271. .68240
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96298. .103976
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78235. .87873
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                                                                                                                                                                                  ordered pieces.
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Pred. No.
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                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                        Hominidae; Homo
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BASE COUNT
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Search completed: April 25, Job time: 719.885 secs
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TITLE
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Best Local :
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                                                                                                  Consensus quality: 158733 bases at least Q40
Consensus quality: 151469 bases at least Q30
Consensus quality: 152087 bases at least Q30
Consensus quality: 152087 bases at least Q20
Estimated insert size: 160000; pulse field gel estimation
Estimated insert size: 162240; sum-of-contigs estimation
Quality coverage: 9.28 in Q20 bases; pulse field gel estimation
Quality coverage: 9.16 in Q20 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
** consists of 6 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** This sequence will be replaced
** This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * the accession number will be preserved.

* 1 85871 contig of 85871 bp in length

* 85872 85971: gap of unknown length

* 85972 96755: contig of 10794 bp in length

* 96866 103302: contig of 6437 bp in length

* 96866 103302: contig of 6437 bp in length

* 103403 103402: gap of unknown length

* 103403 111971: contig of 8569 bp in length

* 111972 112071: gap of unknown length

* 112072 129034: contig of 15963 bp in length

* 112003 129134: gap of unknown length

* 129035 129134: gap of unknown length
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39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 31, 2001 this sequence version replaced gi:9211234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Joint Genome Institute Center Code: JGI
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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AAI79941			AA182407	ABV36584	ABL38444							AAT2221	AAC8923	ABQ692	AAK96733	AAK95240	ABQ67195	ABN83124	AAF28545	ABL12924	ABA21109	AAC68089		AAN70128	AAS62681	AAI94407	ABK80793	ABK43012	AAV89709	AAS87118	AAS87115	ABS11680	AAI43563	AAI18447	AAK37688
Human polynucleoti	prostate				Human colon tumour		Novel human polynu	Human cancer relat	Human ORF3820 cDNA	Thyroid cancer rel	ORFX	Human gene signatu	Human brain T calc	Listeria innocua D	Human neuregulin-1	Human neuregulin-1	Listeria innocua c	Human voltage-acti	Genomic fragment #	Drosophila melanog	Human nervous syst	Human secreted pro	-	Novel DNA encoding	cDNA sequence #468	Human neuroblastom		Genomic sequence #	EST clone CT857.	DNA encoding novel	=	genome		0	Human bone marrow

ALIGNMENTS

RESULT 1
ARCHIP 1
ARCHIP 2
ACC ARCC
XX 06-(
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. WPI; 2000-500381/45. P-PSDB; AAG03788. Dumas Milne Edwards 06-SEP-2000. EP1033401-A2 Homo sapiens Human secreted protein 5' EST, SEQ ID NO: 3792. 06-OCT-2000 AAC03794 standard; cDNA; 447 BP 21-FEB-2000; 2000EP-0200610 (GEST) GENSET 26-FEB-1999; (first entry) 99US-0122487 J, Duclert A, Giordano

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DNA encoding novel
DNA encoding howel
DNA encoding human
DNA encoding human
Human foetal liver
Probe #9118 for ge
Human brain expres

New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond

tag (5' EST) for to 5'ESTs and for

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RESULT 2
AAZ42680
ID AAZ442680
AAZ AAZ4
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DT 01-F
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PRESENTATION OF THE PR
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Best Local Similarity 100.0%;
Matches 111; Conservative 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification; ss.
                                                             Claim 1; Page 402; 837pp; English
                                                                                                                       Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1998;
28-APR-1998;
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AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST
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98US-0069047.
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                                                                                                                                                                                                                                                                                                                              Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC AAY65438 represent the EST related proteins. AAY64651 to CC AAY65438 represent the EST related proteins corresponding to AAY2265 to CAZ43052. The 5 ESTs can be used for producing secreted human gene CC products. They can be used to identify and isolate 5' untranslated Cregions (UTRs) and upstream regulatory regions which control the CC location, development stage, rate, and quantity of protein synthesis, as CC well as stability of mRNA. The ESTs are also useful as probes for CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in CC also be used in forensic procedures to identify individuals, or in CC diagnostic procedures to identify individuals for in CC used for directing extracellular secretion. The products may also be used in CC used for directing extracellular secretion of a polypeptide or the CC insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in CC therapeutic value, and the identifications. Secreted proteins have therapeutic value, and the identification of new secreted proteins is CC valuable. AAZ42249 to AAZ42264 and AAZ64644 to AAZ64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
             Claim 1;
                                                                                                                                 P-PSDB;
                                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #9245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS73441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS73441 standard; cDNA; 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 447 BP; 74 A; 105 C; 125 G; 138 T; 5 other;
                                                                                                                                                    WPI; 2001-639362/73
                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGGCCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                         supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping;
                                                                                                                                 ABG09254
             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                    Liu C,
             NO
                                                                                                                                                                                                                                                                                                                                                                                                                                     e mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder;
           9245; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 111; DB 2
100.0%; Pred. No. 3e-46;
                                                                                                                                                                                    Tang
                                                                                                                                                                                    YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                 mutations
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AAS66674
ID AASI
XX
AC AASI
AC I3-I
DT 13-I
XX
DE DNA
XX
DE DNA
XX
KW Hum
KW FOO
XX
OS Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II), (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. (CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed at the various of the invention.
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 RESULT
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The invention rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS66674 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 660 BP; 149 A; 127 C; 148 G; 236 T; 0 other;
                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #2478.
                                                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001
                                                      Claim 1; SEQ ID No 2478; 103pp; English.
                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                  WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 AAAACTCCTGGGTCTCTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAACTCCTGGGTCTCTGTGTGTG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                 ABG02487.
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                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                           2000US-0540217.
2000US-0649167.
                    relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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 polynucleotide (I) and suseful as hybridisation probes,
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0.017;
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RESULT 5
ABK24383
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK24383 standard; cDNA; 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to novel human lung cancer polynucleotide (I) and polypeptides (II). (I) and (II) are useful in pharmaceutical compositions, such as vaccines, for the diagnosis and treatment of lung cancer. The polynucleotides are also useful as probes or primers for nucleic acid hybridisation. ABK24314-ABK24397 represent human lung cancer coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lung cancer; cytostatic; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding human lung cancer protein, Seq ID
                                                                                                                                                                                               New lung tumour polypeptides and polynucleotides, useful in pharmaceutical compositions, such as vaccines, for treating
                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001; 2001WO-US17066
                                                                                                                            Claim
                                                                                                                                                                         preventing lung cancer, or as probes or primers for nucleic
                                                                                                                                                                                                                                                   WPI; 2002-122068/16
                                                                                                                                                              hybridisation
                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTCATCTTTGCAGGGACTT 2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCATCTTTGCAGGGACTT 51
                                                                                                                          9; Page 172; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2526 BP; 871 A; 536 C;
                                                                                                                                                                                                                                                                                     SL,
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                                                                                                                                                                                                                                                                                                                                                            2000US-207485P
2000US-230475P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                     Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.0%;
100.0%;
                                                                                                                                                                                                                                                                                       Bangur CS,
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Pred. No.
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                                                                                                                                                                                                                                                                                         Klee
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                                                                                                                                                                                                                                                                                       JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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acid
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RESULT 7
ABA63453/c
ID ABA63453
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ABK24390
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
  01-FEB-2002
                                                                                                                                                                The invention relates to novel human lung cancer polynucleotide (I) and polypeptides (II). (I) and (II) are useful in pharmaceutical compositions, such as vaccines, for the diagnosis and treatment of lung cancer. The polynucleotides are also useful as probes or primers for nucleic acid hybridisation. ABK24314-ABK24397 represent human lung cancer coding sequences of the invention.
                   ABA63453;
                                                                                                                                                  Sequence 431 BP;
                                                                                                                                                                                                                          Claim 1; Page 174; 179pp; English.
                                                                                                                                                                                                                                                 New lung tumour polypeptides and polynucleotides, useful in pharmaceutical compositions, such as vaccines, for treating preventing lung cancer, or as probes or primers for nucleic
                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                       WPI; 2002-122068/16.
                                                                                                                                                                                                                                                                                                         Harlocker SL,
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                                                                                                                                                                                                                                              hybridisation
                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200192525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lung cancer; cytostatic; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human lung cancer protein, Seq ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK24390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK24390 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 431
                                                                               18
                                                                                              91 TGCCTGAGTGGCTGCTCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 TGCCTGAGTGGCTGCTCT 108
                                                                              TECCTEAGTEGCTECTCT
                                                                                                                 18;
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                                                                                                                        Similarity
                                   standard;
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                                                                                                               Conservative
(first entry)
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                                                                                                                                                                                                                                                                                                                                         2000US-207485P
2000US-230475P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 108 A;
                                                                                                                                                                                                                                                                                                       Wang T,
                                                                                                                                                108 A; 97 C; 123 G; 101 T; 2
                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 431
                                                                                                                       16.2%;
100.0%;
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G
                                   570
                                                                                                                                                                                                                                                                                                       Bangur CS,
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                                  ВP
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 G; 101 T; 2 other;
                                                                                                               Mismatches
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No.
                                                                                                                                                                                                                                                                                                      Klee JI,
                                                                                                                       DB
17;
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ss.
                                                                                                                               Length 431;
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                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
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acid
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                                                                                                                                              RESULT 8
ABA30652/c
ID ABA306
DЬ
                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                         Query Match
                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                        WO200157274-A2
                                                                                          Probe #9118 for
                                                                                                                              ABA30652;
                                                                                                            23-JAN-2002
                                                                                                                                              ABA30652 standard;
                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                        505 TGTGTGTGCCTGAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                          18;
                                                                                                          (first entry)
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DЪ ş

gene expression analysis in human heart cell sample

DNA;

ВP

488

DX AX

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04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-06323689.
27-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236599.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                      Sequence 570 BP; 169 A; 154 C;
                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 11758; 639pp + sequence listing;
                                                                                                                                                                                                      from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human foetal liver single exon nucleic acid probe #11758.
85 TGTGTGTGCCTGAGTGGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes zing gene expression in human fetal liver -
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                Conservative
                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US00669
                                                                                   16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                0;
                                                              Score 18; DB; Pred. No. 17; 0; Mismatches
                                                                                                                                                   156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                   91 T; 0
                                                                                   DB 22;
17;
                                                              0,
                                                                                                                                                   other;
                                                                                                      Length 570;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful
                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe;
                                                           Gaps
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ID AAK119
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Best Local
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes measuring human gene expression in a sample derived from human hupresent sequence is one such probe. The probes may be used for present sequence is one such probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single
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03-AUG-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 570 BP; 169 A; 154 C; 156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                         Human; brain expressed emicroarray; Alzheimer's
                                                                                                                                                                                                                                                                           AAK11985 standard; DNA; 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                09-AUG-2001.
                                                                                                                      WO200157275-A2
                                                                                                                                            Homo
                                                                                                                                                                epilepsy; cancer;
                                                                                                                                                                                                          Human brain expressed single exon
                                                                                                                                                                                                                                 05-NOV-2001
                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                 505
                                                                                                                                                                                                                                                                                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236839.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                               (first entry)
                                          2000US-0180312
2000US-0207456
                                                                           2001WO-US00667
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                                                                                                                                                                 ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                   16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen
                                                                                                                                                                                     exon;
                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes
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                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                      Score 1
                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for analyzing
                                                                                                                                                                           multiple sclerosis;
                                                                                                                                                                                   expression
                                                                                                                                                                                                          probe SEQ ID NO: 11976.
                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                       No.
                                                                                                                                                                                                                                                                                                                                                                                                                     91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      DB
17;
                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                    analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from human heart.
                                                                                                                                                                         schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                570;
                                                                                                                                                                                    prope;
                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
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Best Local :
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                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                           03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single
brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                              Human; bone
microarray;
                                                                                                                                                                                                                                                                                                                                                AAK37688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                          Human bone marrow expressed
                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes which are derived from genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4;
                                                             WPI; 2001-488900/53
                                                                                                                   04-OCT-2000;
                                                                                                                                                                                          30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                             WO200157276-A2
                 Example
                                                                                                 (MOLE-)
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          505 TGTGTGTGCCTGAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                            85 TGTGTGTGCCTGAGTGGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                  genome-derived single zing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS
                                                                                                 MOLECULAR DYNAMICS INC
                  4;
                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                               Hanzel
                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:
                                                                                                                 2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                       marrow expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 169
                                                                                                                                                                        2000US-0180312
                 ID NO:
                                                                               DK,
                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%;
100.0%;
                                                                                                                                                                                                                                                                 leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11976; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                 12245;
                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                            488
                                                                                                                                                                                                                                                                                                                                                 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes
                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c;
                                            exon
                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                 658pp + Sequence Listing;
                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
                                                                               Rank
                                                                                                                                                                                                                                                                Lymphoma; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for analyzing gene expression in
                                         nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G;
                                                                                                                                                                                                                                                                      gene expression
                                                                                                                                                                                                                                                                                          exon
                                   bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
17;
                                   marrow
                                                                                                                                                                                                                                                                                          probe
                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 570;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                        analysis; probe;
                                                                                                                                                                                                                                                                                          NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                 English
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
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of single

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nucleic

acid

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    Query Match
Best Local S
Matches 18
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118447
                                                                                                                                             The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                           expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI18447 standard;
                                                        Sequence
                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the huma bone marrow. They can be used to measure gene expression in bone marro samples, which may enable the improved diagnosis and treatment of can such as lymphoma, leukaemia and myeloma. The present sequence is one the probes of the invention.
                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                         Penn
                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #8380 for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 570
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                              2001-488901/53.
                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGTGTGCCTGAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGTGTGCCTGAGTGGC 102
                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                           25; SEQ ID No 8380; 487pp; English.
     1 Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; microarray;
                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.
18; Conservative
                                                         570
                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632368.
; 2000US-0234686.
; 2000US-0234685.
; 2000US-02346359.
      Conservative
                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 169 A; 154 C;
                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss.
16.2%; Sc.
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.2%; Suc
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                      A; 154 C; 156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
  Score 18; DB;; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic sequences expressed in the human to measure gene expression in bone marrow improved diagnosis and treatment of cancers
                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                        91 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 T; 0 other;
               DВ
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
17;
                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                        0 other;
    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                           Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                             trom WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
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Indels

0;

Gaps

0

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RESULT 13
ABS11680/c
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                                                                                                                           Qy
                                                                                                           В
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AAI43563/c
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                                                                                                                                             Matches
                                                                                                                                                        Best
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes 
The present sequence is one such probe. The probes are useful for 
producing a microarray for predicting, measuring and displaying g 
expression in samples derived from human placenta. The probes are 
for antenatal diagnosis of human genetic disorders.
       Human genome-derived single
                                                              ABS11680 standard;
                                                                                                                                                                                 Sequence 570
                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                          analyzing
                                                                                                                                                                                                                                                                                                                       Penn
                         19-AUG-2002
                                            ABS11680;
                                                                                                                                                                                                                                                                                                     WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI43563
                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #12249 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI43563;
                                                                                                           505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 TGTGTGTGCCTGAGTGGC
                                                                                                                     85 TGTGTGTGCCTGAGTGGC 102
                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 TGTGTGTGCCTGAGTGGC
                                                                                                         TGTGTGTGCCTGAGTGGC
                                                                                                                                                                                                                                                                         genome-derived single exon nucleic zing gene expression in human placer
                                                                                                                                                                                                                                                         25;
                                                                                                                                              18;
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                      Hanzel
                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                              Conservative
                         (first entry)
                                                                                                                                                                                 BP; 169 A; 154 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                         ID No
                                                                                                                                                                                                                                                                                                                       DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to measure gene expression in human placenta sample
                                                              DNA;
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                                                                                                                                                      16.2%;
100.0%
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                                                                                                           488
                                                              570
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                                                                                                                                                       .08;
                                                                                                                                                                                                                                                      654pp;
                                                                                                                                                                                                                                                                                                                     ξ
                                                              ВP
                                                                                                                                             0;
       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                 156
                                                                                                                                                                                                                                                                                                                      Rank DR
                                                                                                                                              Mismatches
      probe
                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                         placenta
       from
                                                                                                                                                        DB
17;
                                                                                                                                                                                                                                                                            nta -
                                                                                                                                                              22;
       lung
                                                                                                                                                                                                                                                                                  probes
                                                                                                                                             0;
                                                                                                                                                              Length 570;
       SEQ ID
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                  useful
       No 11671
                                                                                                                                             0
                                                                                                                                                                                                             are useful
                                                                                                                                            Gaps
                                                                                                                                                                                                                                     (SENP).
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04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0632468.
03-AUG-2000; 2000US-032366.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ds; single exon probe; asthma; lung cancer; COPD; ILD chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyaline membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis.
                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                               2000US-0632366.
2000US-234687P.
2000US-236359P.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                          2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease;
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Chen W,

Spatially-addressable set of single exon nucleic acid probes, used expression in human lung samples

Claim 1; SEQ ID No 11671; 634pp; English

(a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one probes: Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous scherosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, The invention relates to a spatially-addressable set n relates to a spatially-addressable set of single exon probes for measuring gene expression in a sample derived particularly Of.

not appear

in the printed

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RESULT 14
AAS87115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes,

C polymerase chain reaction (PCR) primers, oligomers, and for chromosome

C and gene mapping, and in recomblant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful in medical

CC the polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

anino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matchės
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS87115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS87115 standard; cDNA;
diagnostic coding sequences of the invention Note: The sequence data for this patent did .
                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                       biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #22919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 570 BP; 169 A; 154 C; 156 G; 91 T;
                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505
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DB; ABG22928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGTGTGCCTGAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGTGTGCCTGAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conserv
                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                     ID No 22919; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΥT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĎΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Length 570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                     mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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20 x 30

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RESULT 15
AAS87118/c
ID AAS87118 standard;
(II). (II) is useful for generating antibodies against it, detecting or contributing a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. As564197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at figure in the printed specification, but was obtained in electronic format directly from WIPO at figure in the printed specification.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromomomer of the polymer of the polymers of the polymers of the polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
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at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABG22931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #22922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 TGCCTGAGTGGCTGCTCT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 TGCCTGAGTGGCTGCTCT 108
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84282 RPCI	284	17	\sim	1	24	44
677950 HS_5	67795	17	- 1	_	24	43
683450 HS_5	68345	17		1	24	42
266658 RPCI	26665	17	1 -1	Ļ	24	41
170366 Pan	17036	17		Ν	25	40
155327 Pan	15532	17	\sim	2	25	39
070759 Pan	07075	17	~	2	25	38
379371 RPCI	37937	17	~	2	25	37
378145 RPCI	37814	17	1.11		25	36
375479 RPCI	37547	17	h 1	.~	25	35
519549 HS_5	51954	17	-		25	34
533287 RPCI	53328	17		2	25	ω ω
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697116 HS_5	69711	17	14		25	<u>ω</u>
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111263 Pan	11126	17	10	w	26	29
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5615 RPCI11	5615	17	~1	ω	26	27
350708 RPCI	3507	17		٠.	27	26
238365 RPCI	2383	17	1 12		27	25
60919 Pan	1609	17	(11		28	24
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136209 HS_5	1362	17	_		28	22
588089 CITB	5880	17	\sim	5	28	21
548294 RPCI	5482	17	~ 1	5	28	20.
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320567 RPCI	3205	17	ш.		س	20
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VERSION KEYWORDS RESULT 1 AQ770688 LOCUS SOURCE ORGANISM COMMENT REFERENCE ACCESSION DEFINITION TITLE MEDLINE JOURNAL AUTHORS AQ770688 470 bp DNA linear GSS 28-JUL-: HS_5368_B2_C08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=944 Col=16 Row=F, DNA sequence. AQ770688 Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Mashington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. library availability, please contact Pieter de Jong Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 470) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a: GSS Homo sapiens AQ770688.1 GI:5648804 Hood, L human. GSS 28-JUL-1999 For BAC and

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ORGANISM
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                                                                                                                                Sequence Tagged Connector Plate: 3025 row: N colu Class: BAC ends
                                                                                                                                                                                                       401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                           High quality sequence stop: 525.
Location/Qualifiers
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HS_3025_B2_G06_T7 CIT
sapiens genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Plate: 944 row: F column: 16
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                                                                                                                                                                                     jwallace@u.washington.edu
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="platte=3025 Col-12 Row=N"
/clone_lib="CIT Approved Human Go
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/sex="male"
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AQ442274
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Best Local
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Best Local
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34 TCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTG 143
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library are derived from
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.com/. BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams,M.D., Rounsléy,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
AQ237815
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45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ237815 628 bp 1
RPCI11-70H4.TK RPCI-11 Homo sapiens
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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ilarity 100.0%;
Conservative
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                                                                                                                                                                RPCI11 Human
150 c
                                                                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
150 c 164 g 189 t
                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="RPCI-11-70H4"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: sperm; Vector:
E-Coli DH10B"
139 c 137 g 143 t
                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                            /db_xref="GDB:7526667"
                                                                                                                                                                                                                                                                                                                             /organism∞"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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                                                                          0;
                                                                      Score 38; DB; Pred. No. 3.5
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Pred. No.
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                                                                                         DB 17;
. 3.5e-09;
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7.7e-1;
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                                                                                                        Length 628
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RPCI-11-70H4, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11.
                                                                                                                               library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)
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35; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.htsc.washington.edu
Plate: 713 row: K column: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99380589
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Mahairas, G.G., Wallace, J.C.,
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AQ442274.1
 Mahairas, G.G., Wallace, J.C., Keller, A., Shaker, R., Furlone
                                                                                              Homo sapiens
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                                                                                                                  numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 410
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 31.5%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Male blood DNA was isolated from one randomly chosen and partially digested with a combination of EcoRI an EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 111 c 111 g 107 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Homo sapiens"
/db_xref="taxon:9006"
/clone="plate=713 Col=23 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB: Pred. No. 1.2
0; Mismatches
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Furlong, J., Young
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hes 0;
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Young, J., Zhao, S.,
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g,J., Zhao,S.,
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 Holzman,
Adams, M.
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99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                              Unpublished (1997)
Other GSSs: CITBL-E1-2544B15.TF
Contact: Shaying Zhao, William I
Department of Eukaryotic Genomic
The Institute for Genomic Reseau
                                                                                                                                                                                                                                                                                                                                                                                 AQ390599 635
CITBI-E1-2544B15.TR CITBI-E1
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35; Conser
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Location/Qualifiers
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.htsc.washington.edu
plate: 713 row: O column: 12
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Clones are derived from the human BAC library
library availability, please contact Pieter de
                                                                                                                                                                             Venter, J.C.
Use of BAC End Sequences
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AQ390599.1 GI:4361622
GSS.
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                                                            9712 Medical Center
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hbe@tigr.org
are available
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a 127 c 117 g 124 t 1 others
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/clone_lib="RPCI-11 Human Male BAC Library"
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/db_xref="taxon:9606"
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Pred. No.
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                                                                                                                William Nierman,
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                                                                                                 Genomics
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Genetics (info@resgen.com).
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FEATURES
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AQ881246/c
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Best Local
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                                                                                                                                                                                                                      Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ881246 529 bp DNA linear GSS 09-NO
HS_5137_B1_F08_T7 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=8905 Col=15 Row=L, DNA sequence.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Natl. Acad. Sci. U.S
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen d and partially digested with a combination of EcoRI and
                                               /clone="Plate=8905 Col=15
/clone_lib="RPCI-11 Human
/sex="male"
                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                            Location/Qualifiers
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/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
144 c 172 g 127 t
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SOURCE

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sapiens genomic

clone

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53 TGGGGCCGGAGTATGTAAAACTCCTGGGTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
AQ420187 5
RPCI-11-185J19.TJ RPCI-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7
Class: BAC ends.
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="GDB:7537944"
/db_xref="taxon:9606"
/clone="RPCI-11"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
121 c 106 g 112 t
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100.0%; Pr
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0; Mismatches
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; Pred. No. 4.20
0; Mismatches
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    Homo
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4.2e-07;
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RPCI-11-185J19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 2
Unpublished (1997)
Other_GSSs: RPCII1-154D6.TV
Other_GSSs: RPCII1-154D6.TV
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,J.C.
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Seq primer: SP6
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Fax: 301 838 0208
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Mammalia; Eutheria; Primates;
                                                                                                             Zhao, S., Adams, M.D., Nierman, W.,
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/db_xref="GDB:7570890"
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/clone="RPCI-11-185J19"
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
BACPAC Genetics (info@resgen.com). BAC end search page:
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                         Email: szhao@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
higher chance of clone tracking errors.
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Other_GSSs: RPCI-11-175G22.TJ
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Class: BAC ends.
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
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/db_xref="GDB:7558829"
/db_xref="taxon:9606"
/clone="RPCI-11-15406"
/clone_lib="RPCI-11"
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/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
165 c 135 g 199 t
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                                                                                                                                                                                                                                                                                                                                                                                             (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
AG179297
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rujayama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library RPCI-43 Unpublished
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Pan troglodytes DNA, clone: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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/db_xref="GDB:7566981"
/db_xref="nexon:9606"
/clone="RPCI-11-175G22"
/clone_lib="RPCI-11"
                                                                              /cell_type="lymphocytes"
/celne_lib="RPCI-43 Chimpanzee Male BAC Library"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
135 c 122 g 192 t 3 others
                                                                                                                                                        /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-051111.TJ"
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
148 c 137 g 158 t
                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                   location/Qualifiers
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27.9%; Score 31; DB 17; 100.0%; Pred. No. 1.6e-05; tive 0; Mismatches 0;
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                                     Length 695;
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AQ207172
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                                                                                                                                                 DNA sequence.
AQ115544
AQ115544.1 G
1 (bases 1 to 399)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RPCI11-57K21.TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Seguence Tagged Connector
Plate: 3239 row: F column: 5
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Nat 99380589
                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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AQ207172
                                                                                                                    human
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Location/Qualifiers
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High Throughput Sequencing Center
University of Washington
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3239 Col=5
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/sex="male"
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Eutheria; Primates; Catarrhini; Hominidae;
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                         Email: mdadams@tlgr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu//ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: RPCI11-57L19.TJ
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1 (bases 1 to 435)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Constant of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence.
AQ116061
AQ116061.1 GI:3492182
GSS.
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
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RPCI11-57L19.TK RPCI-11 Homo
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Other_GSSs: RPCI11-57K21.TJ
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The Institute for Genomic Researc
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Class: BAC ends.
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
a 111 c 95 g 73 t
                Location/Qualifiers
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/clone="RPCI-11-57K21"
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/db_xref="GDB:7521764"
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Best Local
379 GAGTATGTAAAACTCCTGGGTCTCTGTGTG 350
            61 GAGTATGTAAAACTCCTGGGTCTCTGTGTG 90
                                                  30;
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                                                                                                             131
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/clone_lib="RPCI-11"
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/db_xref="GDB:7521786"
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100.0%; F.
                                                            Score 30;
Pred. No.
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Search completed: April 25, 2003, 00:52:48 Job time: 378.284 secs

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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
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US-09-425-043-8

US-09-425-998-4

US-09-425-998-4

US-08-550-715-1

US-09-627-376-3

US-09-627-376-3

US-09-627-376-19

US-08-136-743B-1

US-08-97-166-11

US-08-955-138-3
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US-09-149-476-307
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US-09-233-6061-1
US-09-334-601-6
US-09-334-601-1
US-08-980-102-18
US-08-980-102-18
US-09-334-601-5
                                                                                                                                               US-09-024-020B-1

US-09-425-043-1

US-09-024-020B-2

US-09-425-043-2

US-09-425-043-7

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US-09-425-043-43
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US-09-819-993-3	US-08-772-440-33	US-08-954-441-1	US-08-323-170B-1	US-08-385-335A-9	PCT-US93-02147A-1	US-09-236-503-1	US-08-447-642-1	US-08-284-941-1	US-09-442-100-5	US-08-750-494-3	US-08-468-878-3	US-08-471-733-3	US-08-262-220-3	US-08-750-494-13	US-08-468-878-13	US-08-471-733-13	US-08-262-220-13
Sequence 3, Appli	Sequence 33, Appl		Sequence I, Appli	Sequence 9, Appli		Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 3, Appli	ب -	Sequence 3, Appli	Sequence 3, Appli	Sequence 13, Appl	Sequence 13, Appl	`	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-09-221-017B-1081/c
  TELEFAX:
TELEX: 706141
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
TYPE: nucleic double.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                      FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION ODTA:
APPLICATION UMBER: PCT/AU
APPLICATION UMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONICOY, Gladys H
REGISTRATION NUMBER: 32,43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows Version SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                  REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
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CLASSIFICATION:
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TOPOLOGY:
circular
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US-09-221-017B-1081
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Best Local :
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/0449:
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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09-149-476-307
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HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                  ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/04
ER APPLICATION NUMBER: 60/04
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/04
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 6
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APPLICATION NUMBER: 60/
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/040,334 FILING DATE: 1997-03-07 APPLICATION NUMBER: 60/040,336
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
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APPLICATION NOTICE:
                                                                                                                                                                                                                                         APPLICATION NUMBER: 61
                                                                                                                                                              FILING DATE: 1997-05-23
                                                                                                                                                                             FILING DATE: 1997-0
APPLICATION NUMBER:
                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-03-07
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
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Pred. No.
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15;
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APPLICATION NUMBER: 60/056,637
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APPLICATION NUMBER: 60/056,886
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APPLICATION NUMBER: 60/047,593
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APPLICATION NUMBER: 60/047,501
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SEQTH: 2128
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APPLICANT: Fukuda, Minoru
APPLICANT: Yeh, Jiunn-Chern
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LENGTH: 2178
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
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APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
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               ATTCTTTTTCATCTTT 41
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16; Conserv
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100.0%; Pred. No.
100.0%; Mismatches
                                                                  14.4%;
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                                                                     Score 16;
Pred. No.
                                                        Mismatches
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RESULT 5

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RESULT 6
US-07-746-705A-16
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SEQ ID NO 1
LENGTH: 2288
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APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uery Match
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (29)..(1282)
,09-334-601-1
                                                                                                                  TELEFAX: (301)504-506
TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2915 base pairs
                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2260 ATTCTTTTTCATCTTT 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Matthews, Benjamin F. APPLICANT: Weisemann, Jane M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 19910816 CLASSIFICATION: 435
                                                                                                                                                                                                        NAME: Graeter, Janelle S. REGISTRATION NUMBER: 35,0
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 STRANDEDNESS:
                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Beltsville
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                     cDNA to mRNA
                                                      both
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16
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100.0%; Pred. No.
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                                                Query Match
Best Local Similarity
Matches 16; Conserv
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Sequence 18, Appire
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1977 CTTTGCAGGGACTTCT 1992
                                                                                                                                                    FEATURE:
                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-6629
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2915 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Graeter, Janelle S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1977 CTTTGCAGGGACTTCT 1992
                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                            ANTI-SENSE:
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ADDRESSEE: Janelle S. Graeter
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                         38
                                                                                                                                                                                                                                                                                                                                                                     NAME: Graeter, Janel REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 CTTTGCAGGGACTTCT 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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              CTTTGCAGGGACTTCT 53
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                                                   ilarity 100.0%;
Conservative (
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                                                                                                                                                                Daucus carota
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100.0%; Pr
                                                                14.4%; Score 16; 100.0%; Pred. No.
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Pred. No.
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RESULT 8 US-09-334-601-5/c

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-334-601-5
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
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APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
               TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3467
                                                                                                                                                                                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILLING DATE: 26-FEB-1997
FILLING DATE: 11-FORMATION:
NUMBER: 11-FORMATION:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0.
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ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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STATE: CA
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                                                                                                                                                               NAME: CLARK, JANET P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 16-FEE
                                                                                                                                                REFERENCE/DOCKET NUMBER:
STRANDEDNESS:
                                                                                                        TELEPHONE:
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5. 6030810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SANGAMESWARAN, LAKSHMI
VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HERMAN, RONALD C.
                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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16-FEB-1998
ON: 536
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                               34,799
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                                                                                                                 US-09-425-043-1
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Best Local Similarity 100
Matches 16; Conservative
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                                                                     Query Match
Best Local Similarity
                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                       TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: ::
SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
TYPE: nucleic acid
STEANNETURES: 5501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
5814 GTCTCTGTGTGTGCCT 5799
                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                     TELEPHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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CITY: PALO ALTO
                          80 GTCTCTGTGTGCCT 95
                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-FEI APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
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                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304-1397
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISH, LINDA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERMAN,
                                                          Conservative
                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                               16-FEB-1998
UMBER: US 60/039,447
26-FEB-1997
                                                                                                                                DNA (genomic)
                                                                                                                                                              single
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100.0%; Pr
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                                                                     14.4%;
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                                                                                                                                                                                                                                                                                      R0020B-REG
                                                          0,
                                                                       Score 16;
Pred. No.
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15;
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RESULT 11 US-09-024-020B-2/c

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US-09-425-043-2/c
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                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6007 base pairs
TYPE: nucleic acid
STEANINENESCS. (152)
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                                                                                                                      APPLICANT: HERMAN, RONALD C. APPLICANT: SANGAMESWARAN, L.
                                                  CORRESPONDENCE ADDRESS:
                                                                  NUMBER OF SEQUENCES:
                                                                                      TITLE OF INVENTION:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                        APPLICANT: DELGADO, STEPHEN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: JANET PAULINE CLARK
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              STREET:
                                                                                                                                                                                                                                                                                                                                                             80 GTCTCTGTGTGCCT 95
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STATE: CA
                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CLARK, JANET P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
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PALO ALTO
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94304-1397
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            E: JANET PAULINE CLARK
3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                      DIETRICH, PAUL S.
FISH, LINDA M.
                                                                             SANGAMESWARAN, LAKSHMI
VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SOLIUM CHANNEL I-SUBUNIT AND A SPLIV
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Pred. No.
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                                                                              I-SUBUNIT AND A SPLICE VARIANT THEREOF
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RESULT 13
US-09-024-020B-7/c
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/024,020
APPLICATION NUMBER: US 60/039,447
APPLICATION NUMBER: US 60/039,447
EILING DATE: 26-FEB-1997
ATTORNEY_AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                            APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DIETRICH, PAUL S. APPLICANT: FISH, LINDA M. APPLICANT: HERMAN, RONALD C.
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                              STREET: 3401 HII
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 94304-1397
APPLICATION NUMBER: US 60/039,447 FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                             ADDRESSEE: JANET PAULINE CLARK
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REGISTRATION NUMBER: 34,799
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ZIP: 94304-1397
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799

R0020B-REG

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US-09-425-043-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNING COUNTY COUNTY THE COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COUNTY CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6556 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Applic Patent No. 6335172
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                                                                                                                                                                   TELEFAX: (650) 855-532 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                      TELEPHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 16-FEB-
APPLICATION NUMBER: 1
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ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SANGAMES TITLE OF INVENTION: TITLE OF INVENTION:
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       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; hes 16; Conservation
                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: JANET PAULLING CHARM.
STREET: 3401 HILLVIEW AVENUE, MS A2-250
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                                                                                                                                   LENGTH:
                                                                                                   nucleic acid
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISH, LINDA M.
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                                       linear
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UMBER: US 60/039,447
DNA (genomic)
                                                                   single
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1 855-5322
2 NO: 7:
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Search completed: April 25, 2003, 00:54:06 Job time: 19.1361 secs
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CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039,447

FILING DATE: 26 FEB-1997

ATTORNEY/AGENT INFORMATION:

""ME: CLARK, JANET P.

34,799
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                                                                                                                Best Local Similarity
Matches 16; Conserv
                                                                                                                                             Query Match
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Best Local
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                                                                                                                                                                                                                                                                            TELEFAX: (650) 855-5322 INFORMATION FOR SEQ ID NO: '
                                                          5991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-FEB-19:
                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: ROTELECOMMUNICATION INFORMATION: TELEPHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                        80 GTCTCTGTGTGTGCCT 95
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 94304-1397
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TOPOLOGY: lir
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                                                                                                                                                                                                                                               6586 base pairs
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SOLIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
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DIETRICH, PAUL S
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                                                                                                                Conservative
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                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      DNA (genomic)
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100.0%; Pr/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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8 172637
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10 US-09-864-761-99118

10 US-10-092-154-1899

10 US-09-774-307-8084

10 US-09-974-300-8084

10 US-09-805-458A-3

10 US-09-805-458A-3

10 US-09-975-668-1

10 US-09-795-668-1

10 US-09-795-668-1
  US-09-964-824A-385
US-10-046-935-2033
US-09-878-178-2033
US-01-146-502-2033
US-10-146-502-2033
US-10-060-036-985
US-10-060-036-985
US-10-09-918-995-26108
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5304.628 Million cell updates/sec
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Sequence 1, Appli
Sequence 87, Appl
Sequence 87, Appl
Sequence 9118, Ap
Sequence 1899, Ap
Sequence 1899, Ap
Sequence 1894, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
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	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4
	2340	2340	2319	2287	2268	2229	2147	2108	2017	2002	1009	997	805	805	805	805	747	557	557	552	548	524	497	494	481	447
	9	9	10	10	9	10	9	10	9	10	10	9	9	9	9	9	12	10	10	10	10	10	10	9	10	10
	US-09-966-262-51	US-09-984-245-51	US-09-874-390-1	US-09-764-864-473	US-10-102-806-142	US-09-925-297-337	US-09-981-353-43	US-09-797-207-3	US-10-102-806-137	US-09-925-300-592	US-09-764-864-12	US-09-809-391-307	US-10-143-090-106	US-09-983-966-106	US-09-966-262-106	US-09-984-245-106	US-10-001-879-101	US-09-764-877-3495	US-09-764-877-746	US-09-998-598-1325	US-09-864-761-12421	US-09-797-207-5	US-09-864-761-1356	US-09-918-995-20796	US-09-560-863-45	US-09-880-107-871
•	Sequence 51, Appl	Sequence 51, Appl	Sequence 1, Appli	Sequence 473, App	Sequence 142, App	Sequence 337, App	Sequence 43, Appl	Sequence 3, Appli	Sequence 137, App	Sequence 592, App	Sequence 12, Appl	Sequence 307, App	Sequence 106, App	Sequence 106, App	Sequence 106, App	Sequence 106, App	Sequence 101, App	Sequence 3495, Ap	Sequence 746, App	Sequence 1325, Ap	Sequence 12421, A	Sequence 5, Appli	Sequence 1356, Ap	Sequence 20796, A	Sequence 45, Appl	Sequence 871, App

ALIGNMENTS

US-09-263-959-1/c

Sequence 1, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:

Hood, Leroy E

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Query Match
                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Howen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNBY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 98104-7092
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                                                                                                            LENGTH:
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                                                      linear
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                                                                                                                                                                                    (206) 622-4900
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 Score 33;
 DB 10;
Length 684973;
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100.0%;

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; OTHER INFORMATION: n = A, T, C or G US-09-866-562-87
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                                                                                                                                       NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
LENGTH: 431
TYPE: DNA
ORGANTON
   Best Local Similarity Matches 18; Conserv
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                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/866,562 CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 210121.502
CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
                                                                                                                                                                                                                                                                                                                          APPLICANT: Harlocker, Susan L.
APPLICANT: Wang, Tongtong
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APPLICANT: Klee, Jennifer
APPLICANT: Switzer, Anne
                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: 361,431
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TYPE: DNA
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                                                                                                                                ORGANISM: Homo sapiens
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LOCATION: 361,431
OTHER INFORMATION: n = A,T,C or
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mes 18; Conservative
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                                                                                                                                                                                                                                                                                                            Bangur, Chaitanya S
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Bangur, Chaitanya S.
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             16.2%; Score 18; 100.0%; Pred. No.
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Pred. No.
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US-09-864-761-9118
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SEQ ID NO 9118
LENGTH: 570
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                                                                                                                                                                           TYPE: DNA
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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OTHER INFORMATION: MAP TO APO00053.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7

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OTHER INFORMATION: EXPRESSED INFORMATI
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Pail See ID NO 1899
LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapiens
US-09-974-300-8084/c; Sequence 8084, Application US/09974300; Patent No. US20020146721A1; GENERAL INFORMATION:
APPLICANT: Berka, Randy M.; APPLICANT: Clausen, Ib Groth; TITLE OF INVENTION: Methods for Monito
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publication No. US20030054375Al
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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Best Local
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                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1899
LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PCO09 CURRENT APPLICATION NUMBER: US/09/764,847 CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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17; Conserv
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100.0%;
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Best Local Similarity
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; Sequence 468, Application US/09822830A
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                                                                                                                                                                                                                                                                                                                                             US-09-822-830A-468
                     GENERAL INFORMATION:
APPLICANT: YAN, CHUMHUA et al
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8884
                                                                                                             Sequence 3, Application US/09805458A Patent No. US20020042100A1
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 468
LENGTH: 1047
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PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06
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CURRENT APPLICATION NUMBER: US/09/822,830A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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FILE REFERENCE: CL000722
CURRENT APPLICATION NUMBER: US/09/805,458A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
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Agostino, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark, Hilary
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: LOCATION: (1)...(172637)
: OTHER INFORMATION: n = A,T,C or G
US-09-805-458A-3
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Best Local Similarity
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulther, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
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PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
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PRIOR FILING DATE: 2001-02-28
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SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
                                                                        NAME/KEY: misc_feature LOCATION: (1)...(1531) OTHER INFORMATION: w=a
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LOCATION: (1)...(1531)
OTHER_INFORMATION: m-a or
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OTHER INFORMATION: s=g
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LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
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OTHER INFORMATION: y=t/u
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LOCATION: (1)...(1531)
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ORGANISM: Human
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RESULT 11
US-09-795-668-1
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US-09-946-807-1
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Best Local Similarity 100.
Matches 17; Conservative
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PRIOR FILING DATE: 2000-02-28
NUMBER OF OF OF OTHER PRIOR PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
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APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
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OTHER INFORMATION: w=a
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OTHER INFORMATION: d=a
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OTHER INFORMATION: b=g
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OTHER INFORMATION: k=g
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Best Local Similarity
Matches 17; Conserv
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LOCATION: (1)...(1531)
OTHER INFORMATION: n=a
-09-795-686-1
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CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
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LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g
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OTHER INFORMATION: v-a
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                                                                                                               ; ORGANISM: Homo sapiens US-10-046-935-2033
                                      Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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LENGTH: 281
TYPE: DNA
ORGANISM: Homo sapiens
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SOFTWARE: FSSTSEQ for Windows Version 4.0
SEQ ID NO 2033
LENGTH: 374
TYPE: DNA
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Patent No. US20020156011A1
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.527C1
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jiang,
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SOFTWARE: PatentIn version 3.0
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108 GATCTTTTGCCTTGCA 123

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RESULT 15
US-09-878-178-2033

Sequence 2033, Application US/09878178

Petent No. US20020177552A1

GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIRAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION UNUMER: US/09/678,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FRASTSEQ for Windows Version 4.0
TYPE: DNA
ORGANISM: Homo Sapien
US-09-878-178-2033

Query Match
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: April 25, 2003, 02:09:14

Job time: 1043.77 secs
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Minimum DB
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ő Score Match Query 5 169620 1 123779 1 123779 1 128118 1 1285818 1 128589 1 148290 1 165649 1 178650 1 192826 124271 146671 159747 162740 162740 175466 1169772 175466 207408 207408 2075408 135090 108040 134760 146059 171347 172206 172567 Length DB \circ AC076969 AC107979 AC107979 AC103996 AC104303 AC0907452 AC0907452 AC0925179 AC025179 AC00101814 AP001019 AC034249 AC05538 AC068875 AC0687283 AC087283 AC087283 AC022294 AC022294 AP001078 AC015793 AC079737 AC025420 AC099484 AC099176 AC099176 AC099176 AC099176 AC099176 AC099179 AC0909980 AC0909980 AC0909980 AC09099980 AC09099980 AC09099980 AC09099980 AC09099980 AC09099980 AC09099980 AL607077 AL691517 H AC092285 HSDJ60101 AL365267 ALIGNMENTS AC025179 Homo sapi AC00814 Homo sapi AP001019 Homo sapi AC034249 Homo sapi AC034249 Homo sapi AC069538 Homo sapi AL607077 Human DNA Continuation (3 of AC068815 Homo sapi AC087283 Homo sapi AC087283 Homo sapi AL09028 Homo sapi AL09028 Homo sapi AL091791 Human DNA AC02224 Homo sapi AP001793 Homo sapi AP001793 Homo sapi AP015676 Homo sapi AC015676 Homo sapi AC01937 Homo sapi AC01937 Homo sapi AC01931 Homo sapi AC01931 Homo sapi AC01931 Homo sapi AC01931 Homo sapi AC103996 Homo sapi AC104303 Homo sapi AC090762 Homo sapi AC0907445 Homo sapi AL358817 Human DNA AC007445 AL358817 AC025179 AC008814 AP001019 AC07637 AC026324 AC068150 AC068150 AC099484 AC099170 AC099776 AC092119 AC092375 AC104687 AC104687 AC092375 AC092375 AC092375 AC092375 AC092375 AC092375 AC076969 Homo sapi AC121249 Homo sapi AC107979 Homo sapi AC012674 Homo sapi AL137847 Human DNA AC021025 Homo sapi Description AL365267 Homo sapi Homo sapi

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REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AC012674/c	RESULT 1
<pre>1 (bases 1 to 169620) Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens.	HTG; HTGS_PHASE1; HTGS_DRAFT.	AC012674.10 GI:9719580	AC012674	18 unordered pieces.	Homo sapiens chromosome 3 clone RP1-458H3, WORKING DRAFT SEQUENCE,	AC012674 169620 bp DNA linear HTG 07-SEP-2000		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Contact: hgsc-help@bcm.tmc.edu
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Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 17, 2001 this sequence version replaced gi:16408610.
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143372)
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                                                                           Kimberley, A.
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                                                                                                                                                                                                      RP11-439K3 on chromosome 9q22.2-31.1,
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RESULT 3
AC021025/c
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Best Local :
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                        Eukaryota;
                                                      Homo sapiens (human)
                                                                                                                                                    Homo sapiens unordered pie
                                                                                                                                                                                                                                     08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                     AC021025
                                                                                                                                                                                                                                                              14-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers give in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-439K3 is from the library RP0I-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations \boldsymbol{\theta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sections only once, except for a short overlap.
The true left end of clone RP11-439K3 is at 1 in this sequence. The true left end of clone RP11-344L17 is at 141373 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RP11-439K3 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
  Primates;
                                                                                                                                                       pieces
                                                                                                                                                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                               chromosome 3 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-439K3"
/clone_lib="RPCI-11.2"
30224 c 28152 g 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="q22.2-31.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                 HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .143372
Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%;
100.0%;
                                                                                                                                                                                                                                Last updated, Version 11)
                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48;
Pred. No.
                                                                                                                                                                                  RP11-79K17, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42187
                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; L
. 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 143372;
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                                                                                                                                                                                  SEQUENCE,
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ORIGIN

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RA BOUCK J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J.,
RA Carter M., Chacko J., Chen Z., COX C., David R., Delgado O., Deshazo D.,
RA Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,
RA Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,
RA Ferraguto D., Forcum-Tansey J., Frantz P., Ganesh R., Gorrell J.H.,
RA Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,
RA Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,
RA Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,
RA Liu J., Liu W., Logan O., Lozado R.J., Lucier R., Martin R.,
RA Liu J., Liu W., Logan O., Lozado R.J., Lucier R., Martin R.,
RA Martinez C., McLeod M.P., Mei G., Morgan M., Morris S., Nash S., Nelson A.,
RA Nguyen R., Nguyen N., Nguyen S., Oswal G., Parish B., Paxton S., Payton B.,
RA Perez L., Pu L.L., Quiles M., Reiter D., Rives M., Samuel S., Say J.,
RA Scherer S., Shah E., Shen H., Simon M., Sparks A., Stamps A., Sucgang R.,
RA Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,
RA Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,
RA Wren J., Wrensford G., Yu W., Zhou X., Nelson D., Gibbs R.;
"The Chilich Called T. The Company C. The Compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 112332 bases at least Q40
Consensus quality: 117272 bases at least Q30
Consensus quality: 119789 bases at least Q30
Estimated insert size: 121963; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JAN-2000) to the EMBL/GenBank/DDBJ databases. Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence of the pieces

* consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny D.M., Adam
Bouck J., Bowie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: HMXB
Center clone name: RP11-79K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center co
Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley K.C.;
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                                                                                                                                                                                                                                                                                                                          runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
    35932
360755
60855
71668
71768
84827
96722
96822
105595
1105695
113008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.hgsc.bcm.tmc.edu/
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105694:
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96721:
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                                                                                                                    g of 13059 bp in f unknown length g of 11795 bp in f unknown length
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of 8773
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of 7191
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of 7213
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of 24723 bp
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SOURCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 123779 BP; 37802 A; 24017 C; 23437 G; 37612 T; 911 other;
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                                                                                           Benton, J., Binage, K., Blankenburg, K., Bennin, D., Bouck, J., Benvin, J., Bilankenburg, K., Bennin, D., Bouck, J., Bowle, S., Briewa, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Defecrich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Eccito, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabssi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jakes, M., Holloway, C., Joudah, S., Karlsson, E., Kelly, S., Huber, J., Hulyk, S., Hume, J., Jakes, M., Jakes, M., Jakes, M., Landry, N., Leal, B., Levis, L.C., Lewis, L., Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiser, A., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Maller, G., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Miner, G., Miner, G., Mitchell, T., Mohabbat, K., Mogupen, A., Mguyen, N., Nickerson, E., Nwokenkwo, S., Martinez, E., Pull, L., Quiles, M., Stanley, H., Shooshtari, N., Sisson, I., Sodergre, E., Sonaike, T., Sparks, A., Tamerisa, K., Tamerisa, K., Stott, G., Scherer, S., Sostt, G., Scherer, S., Sostt, G., Schere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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122221
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                Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 10.1%; Sc
Similarity 100.0%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC076969.6 GI:16117967
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 128118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122220: contig of 1922 bp in length 122320: gap of unknown length 123779: contig of 1459 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="3"
/db_xref="taxon:9606"
/organism="Homo sapiens"
/clone="RP11-79K17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Williams, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 30;
; Pred. No. 2.1e-12;
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e 3 clone
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  Williamson, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length.
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RP11-79K12, WORKING DRAFT SEQUENCE,
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Wleczyk, R.,
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                                                                                    Tamerisa, K.,
                                          Vinson, R.
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AUTHORS
TITLE
                                                                                                         FEATURES
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JOURNAL
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                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA On Oct 14, 2001 this sequence version replaced gi:10047573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 128118)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center clone name: RP11-79K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine Center code: BCM
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                /db_xref="taxon:9606"
/chromosome="3"
                                                          /organism="Homo
                                                                                                       Location/Qualifiers
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.28118: contig
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g of 2950
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y of 6170
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g of 7324
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of 9542 bp in
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of 13212 bp in length
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AC121249/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 128583)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Phelps,K.A., Buckley,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-MAY-2002) Genome Center,
Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Box 352145, Seattle, WA 98195, USA
On May 16, 2002 this sequence version replaced gi:9719675
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AC121249 AC021025
                                                                Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to qual:
                                                                                                                                                                      Overlapping Sequences:
5': RP11-147N17 (UWGC:bc0267) AC104300, 22116-bp overlap
3': RP11-391P4 (UWGC:bc0402) AC104303, 114502-bp overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-JUN-2002) Genome Center, University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Haugen, E.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saenphimmachak, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaul, R.K., Olson, M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uman.
                                             Quality levels above 40 are expected to have less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35433 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 128583)
                       error in 10,000 bp.
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                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; 45% of reads Sequencing vector: M13; L08821; 55% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 128548 bases at least Q40 Consensus quality: 128590 bases at least Q30 Consensus quality: 128591 bases at least Q30 Consensus quality: 128593; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: chr-3
Center clone name: RP11-79K17 (bc0196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Code: UWGC Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: University of Washington Genome Center
                                                                                                                                                                                                                                                                         Quality coverage: 13.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No.
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e 3 clone RP11-79K17, complete sequence.
values are not generally visible from
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Kibukawa, M., Raymond, C.
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Kibukawa,M., Ray
                                                                    quality
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GenBank flat file format but are available as part of this entry's ASN.1 file.

quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction diges: This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Ph quality >= 30); an attempt was made to resolve all sequencing digest. Phred

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. NSiI BglII

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RESULT 6 AC107979/c LOCUS LOCUS DEFINITION AC107979 ACCESSION AC107979 VERSION KEYWORDS HTG. ORGANISH HOmo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE REFERENCE 1 (bases 1 to 148290) AU107979.7 REFERENCE AUTHORS HOmo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 148290) Birren, B., Nusbaum, C. and Lander, E.	Count 37777 a 24752 c 24789 g 41265 t [Count 10.1%; Score 40; DB 9; Length 128583; Best Local Similarity 100.0%; Pred. No. 2.1e-12; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 69 AAAACTCCTGGGTCTCTGTGTGTGTGTGTGGCTGAGTGGCTGCTCT 108 [] [] [] [] [] [] [] [] [] [] [] [] [] [7158 7158 7926 1199 1199 11065 1065 749 749 749 1651 1651 1651 1651 1651 1651 1651 1672 4522 1872 4522 1872 1872 6000 1872 1873	1 1 2 0 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2
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FEATURES
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Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 26, 2002 this sequence version replaced gi:21321840. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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mes 40; Conserv
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Homo sapiens chromosome 15, clone RPI1-76E17, complete sequence.
AC103996
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2 (bases 1 to 165649)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
                                                                     Homo sapiens chromosome 15, clone RP11-76E17 uppublished
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Birren,B., Nusbaum,C. and Lander,E.
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2.1e-12;
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Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Johnson, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
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Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Yopham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Submitted (nincolor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (26-2008) (CE 4 (bases 1 to 165649) (CE 4 (bases 1 to 165649) (CE 5 Earna, N., Bastlen, V., Bloom, T., Boyuslavkiy, L., Boukhgalter, B., Barna, N., Bastlen, V., Bloom, T., Boyuslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Ind, R., Nice, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
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Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,

Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreita, P., FitzGerald, M., Gage, D., Galagan, J.,

Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,

Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,

Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,

McCarthy, M., Mells, C., Landers, T., Levine, R., Milenga, V.,

Murphy, T., Naylor, J., Nuyuen, C., Nicol, R., Norbu, C., Norman, C.H.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Vong, G., Zainon, T.
                                                                                                                                                                                                                                                          Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma (02141, USA On Jul 1, 2002 this sequence version replaced gi:21592191. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                          Smit, A.F.A. & Green, P. (1990-1997)
http://ftp.genome.washington.edu/Rm/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
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RENCE DURNAL

REFERENCE TITLE JOURNAL

AUTHORS

COMMENT

/rpt_family="AT_rich"

JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                         /rpt_1
19211.
                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_fami
7354. .76
                                                                                                                                       /rpt_family="L1PA4"
18155. .19210
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19483. .19546
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7214. .7319
                                                                                                                                                                                                 complement (15218.
                                                                                                                                                                                                                                 15036
                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="LlPA10"
complement(7745. .78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5650. .6330)
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                                                                                                                                                                                                                /rpt_family="L1MC3"
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complement///c"
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                                                                                                                                                                                                                                                             'rpt_family="(TA)n"
.4507. .15032
                                                                                                                                                                                                                                                                                                                                                                 rpt_family="AluSp/q"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L2"
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                                                                                                                                                                                                                                                                                           14503
                                                                             19372
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KEYWORDS
SOURCE
ORGANISM
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INITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8110 TAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTC 8071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 40; Conserva
                                                                                                                                                                                                                                                                                                                    178650 bp DNA linear PRI 25-FBE HOMO Sapiens chromosome 3 clone RP11-391P4, complete sequence. AC104303 AC064830 AC104303.2 GI:18874945
                                                                       Submitted (07-DEC-2001) Genome Box 352145, Seattle, WA 98195, 3 (bases 1 to 178650)
Submitted (25-FEB-2002) Genome Center, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 178650)

Raul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
                               Direct Submission
                                         Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Phelps, K.A., Raymond, C.
                                                                                                                             Direct Submission
                                                                                                                                   2 (bases 1 to 178650)
Kaul, R.K., Olson, M.V., Raymond, C. and
                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                       Homo sapiens.
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complement(29673.
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complement(27659..27811)
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complement(21943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                            Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1e-12;
hes 0;
                                                                                                                                        Haugen, E.D.
               University of Washington
                                                                                                          University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 165649;
                                             and Haugen, E.D.
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COMMENT
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality and the phrap assembly program.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phre quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Overlapping Sequences:
5': RP11-475023 (UWGC:bc0439) AC023346
3': RP11-79K12 AC076969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On
                                                                                                                                                                                                                                                                                                                                                 SeqDerMap
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Validation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality levels above 40 are expected to have 1 error in 10,000\ \mathrm{bp}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feb 25, 2002 this sequence version replaced gi:17402782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: unknown; 55% of reads Sequencing vector: plasmid; 45% of reads Chemistry: Dye-terminator ET; 89% of reads Chemistry: Dye-terminator Big Dye; 11% of reads Chemistry: Dye-terminator Big Dye; 11% of reads Chemistry: 17649 bases at least Q40 Consensus quality: 178631 bases at least Q30 Consensus quality: 178631 bases at least Q20 Insert size: 178648; sum-of-contigs
                                                                                                                                                13472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: chr-3
Center clone name: RP11-391P4 (bc0402)
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 8.0x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drafting Center: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Code: UWGC
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RESULT 10
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Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
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Wheeler, J., W., Wann, D., Ye, W.J., and Zodv, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                 On Jun 30, 2000 this sequence version replaced gi:8705092 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                Submitted (30-APR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 32918)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-344B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 18 clone RP11-344B7 map 18, IN PROGRESS ***, 1 ordered piece.
                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                               Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
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AC007445.5 GI:8844149
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36682.
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/rpt_family="AluSx"
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complement/2007
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complement/35/10
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Institute/ MIT Center
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Pred. No. 2.1e-12;
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                                                                                                                requests: clonerequest@sanger.ac.uk

on Oct 9, 2001 this sequence version replaced gi:14669268.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
                                             assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (06-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone RP11-399N22 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Conserv
                             SWISSPROT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete sequence. AL358817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available and the accession number will be preserved. . 1 32918; contig of 32918 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR Web site: http://www-seq.wi.mit.edu
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1. .32918
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/map="18"
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found at
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Pred. No.
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. 8.2e-12;
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                        on the WORMPEP
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REFERENCE
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Estimated insert size: 117160; agarose-fp estimation Estimated insert size: 123571; sum-of-contigs estimation Quality coverage: 6.46 in Q20 bases; sum-of-contigs estimation Quality coverage: 6.12 in Q20 bases; sum-of-contigs estimation * NOTE: This is a 'working draft' sequence. It currently
                                                                                                            Consensus quality: 116609 bases at least Q40 Consensus quality: 120226 bases at least Q30 Consensus quality: 121274 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert RP11-399N22 It may be shorter because we sequence sections only once, except for a short overlap. The true left end of clone RP11-432J9 is at 36937 The true right end of clone RP11-91A1 is at 2000 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr10
RP11-399N22 is from the library PRCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at
                                                                                                                                                                                                                            Center Project Name: 694394
Center clone name: CITB-H1_2174B5
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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                                                                                                                                                                                      Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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DOE Joint Genome Institute
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/clone_lib="RPCI-11.2"
9079 c 9111 g 11431
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/chromosome="10"
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                                                                         Drive, Walnut Creek, CA 94598, USA
On Oct 31, 2001 this sequence version
Draft Sequence Produced by DOE Joint (
                                                                                                                                                                                                                                                                                                                                                                                              HTG.
              www-shgc.stanford.edu
Quality: Phrap Quality
                                                                                                                                                                                 Submitted (03-AUG-1999) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 146671)
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                                                                                                                           Submitted (31-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
                                                                                                                                        Direct Submission
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AC008814
                                          Finishing Completed at Stanford Human Genome Center
                                                            www.jgi.doe.gov
                                                                                                                                                       DOE Joint Genome Institute and Stanford Human Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved
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16: contig of 9333 bp in length
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6: gap of unknown length
2: contig of 14906 bp in length
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                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                      preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in DataBase (2000) 2 (bases 1 to 159747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 159747) 2 (bases 1 to 15974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 31, 2000 this sequence version replaced gi:6997769
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                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 145356 bases at least Q40 Consensus quality: 152272 bases at least Q30 Consensus quality: 155843 bases at least Q20 Insert size: 157447; sum-of-contigs
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Center project name: HumDraft18
Center clone name: RP11-752I11
                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 4.51x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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Pred. No. 8.6e-12;
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* NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence updated (26-May-2000)
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122789: contig of 5823 bp in length
122889: gap of 100 bp
127665: contig of 4776 bp in length
                  151343: gap of 
153454: cont:
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158090 158189: gap of 100 bp
158190 159747: contig of 1558 bp in length
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                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                           * the accession number will be preserved.

1 85871 sap of 85871 bp in length

* 85872 85971; app of unknown length

* 85972 96765; contig of 10794 bp in length

* 96866 103302; contig of 6437 bp in length

* 96866 103302; contig of 6437 bp in length

* 103403 101402; gap of unknown length

* 103403 111971; contig of 8569 bp in length

* 111972 129034; contig of 16963 bp in length

* 112072 129034; contig of 16963 bp in length

* 129035 129134; gap of unknown length

* 129035 129134; gap of unknown length

* 129035 129134; gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 158733 bases at least Q40
Consensus quality: 161469 bases at least Q30
Consensus quality: 162087 bases at least Q20
Consensus quality: 162087 bases at least Q20
Estimated insert size: 160000; pulse field gel estimation
By the coverage: 9.28 in Q20 bases; pulse field gel estimation
Quality coverage: 9.28 in Q20 bases; pulse field gel estimation
Quality coverage: 9.16 in Q20 bases; sun-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 31, 2001 this sequence version replaced gi:9211234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Center Project Name: 570398
Center clone name: RPCI-11_427C17
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Sequencing of Human Chromosome
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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DOE Joint Genome Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           provided by the submittor. This sequence will be replaced
                                                                                                                       48722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 162740)
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ilarity 100.0%;
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                                                                                                                  /clone="RP11-427C17"
/clone_lib="RPCI human BAC
31435 c 31563 g 50520 t
                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                           /chromosome="5"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Mismatches
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    Gaps
    0;
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Db 3599 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGT 3637
Search completed: April 25, 2003, 00:41:44
Job time: 1748.12 secs

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OM nucleic - nucleic search, using sw model
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AAZ42680
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Human 5' EST isola
DNA encoding novel
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Interferon pseudo-
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RESULT 1 AAC03794

ALIGNMENTS

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4.3	4.3	4.3	4.3	4.3		4.3	4.3								4.5			4.5															4.8	4.8	4.8
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AAH69668	AAH70408	AAH73108	AAC70671	AAC70668	AAC70656	AAC70650	AAC70647	AAV89709	ABL34174	ABN60009	ABA09581	AAK85825	ABA09665	AAK85823	AAS87118	AAC79760	AAI94266	AAI94104	AAS87115	ABS11680	AAI43563	AAI18447	AAK37688	AAK11985	ABA30652	ABA63453	AAI83964	ABK24390	ABK24383	AAZ43080	0	ABL28930	ABL09112	08	AAX84949
Human cervical can	Human cervical can	Human cervical can	Single nucleotide				Single nucleotide	0	Human immune syste	Novel human coding	Human bone marrow	Human immune/haema	Human		DNA er		Human	Human neuroblastom	DNA encoding novel	Human genome-deriv	Probe #12249 used	Probe #8380 for ge	Human bone marrow	Human brain expres	Probe #9118 for ge	Human foetal liver	Human polynucleoti	DNA encoding human	DNA encoding human	C. elegans insulin	21-hydroxylase fra	Drosophila melanog		Human secreted pro	Human secreted pro

06-OCT-2000 (first entry) AAC03794 standard; cDNA; 447 BP gene therapy; chromosome mapping; ss. Human secreted protein 5' EST, SEQ ID NO: AAC03794; 21-FEB-2000; 2000EP-0200610 06-SEP-2000 EP1033401-A2. Homo sapiens. Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; 3792.

a

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

WPI; 2000-500381/45. P-PSDB; AAG03788.

Dumas Milne Edwards

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Duclert

A,

Giordano

26-FEB-1999;

99US-0122487.

(GEST) GENSET

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ARESULT 2
ARZ4260
ID ARZ44
XX ARZ4
AC ARZ4
XX ARZ4
DT 01-F
DT 01-F
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                                                                                                                                                                  gene therapy; chromosome mapping; upstream regulatory
forensic; location; development; protein synthesis; st
                                                                                                                                                                                                                                                                                                                                       01-FEB-2000
                          W09953051-A2
                                                                               Homo sapiens
                                                                                                                                       regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ42680 standard;
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                                                                                                                                                                                                                    5' EST;
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                                                                                                                                                                                                                                                                         EST isolated from a cDNA library SEQ ID NO:439.
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                                                                                                                                                                                                                 expressed sequence tag; secreted protein; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA;
                                                                                                                                                         development; protein synthesis; stability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 396; DB 21; 100.0%; Pred. No. 1.8e-183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 447 BP; 74 A; 105 C; 125 G; 138 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences, corresponding to human secreted proteins. AAX64651 to AAX65438 represent the EST-related proteins corresponding to AAX42265 to AAX4634382. The 5' ESTs can be used for producing secreted human gene products. The year be used to identify and isolate 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedu
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28-APR-1998;
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GGTCAGTCCATTGTGRGAMCTGGATATTTCAGTTGA
                                                                 TGGGCGGGCGATTGCCCCTACCCCATTTTTCTTCATTCTCTGTGGGTCAAGDBGTTCACTT
                                                                                                                                    CCTGATCTGTGGGTTGCAAAGATCTGTGGGAGAAGTGTGGTTTCCTGGATGGGGTCACAC
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                                                                                                                  CCTGATCTGTGGGTTGCAAAGATCTGTGGGAGAAGTGTGGTTTCCTGGATGGGGTCACAC
                                                 TGGGCGGCGATTGCCCCTACCCCCATTTTTCTTCATTCTCTGTGGGTCAAGDBGTTCACTT
                                                                                                                                                                                                                                                                                                                                                                                       ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCCG
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98US-0069047
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Pred No. 1.8e-183;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                             Sequence
                 197 CAAAGATCTGTGGGAGAAGTGTGGTTTCC 225
                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                             966 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0540217
2000US-0649167
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                                                                                                                                               250 A; 221 C; 259 G; 236 T; 0 other;
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                                                                                       Score 29;
Pred. No.
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AAS73441/c
ID AAS734
AC AAS74
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Best Local Similarity
Matches 24; Conserv
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
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                                                                                                                                                                                                                                                                          Sequence
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                                    69 AAAACTCCTGGGTCTCTGTGTGTG 92
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                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                      149 A; 127 C; 148 G; 236 T; 0 other;
                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                        0;
                                                                                                                                                                            Score 24;
Pred. No.
                                                                                                                                        Mismatches
                                                                                                                                                                                0.076;
                                                                                                                                                                                                         DB 23;
                                                                                                                                        0;
                                                                                                                                            Indels
                                                                                                                                            0;
                                                                                                                                            Gaps
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RESULT 5 AAN60204

AAN60204;

AAN60204 standard; DNA; 3659

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PA XXX PA PA XXX PA XXX
       RESULT 6
ABK83566/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
              rheumatoid arthritis; glomerulonephritis; asthma; thrombos cardiac reperfusion injury; renal reperfusion injury; ARDS adult respiratory distress syndrome; inflammatory bowel distriction, a disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2557
    granulocyte
                                                                                                             viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                    14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                             ABK83566 standard; cDNA; 147724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3659 BP; 796 A; 885 C; 1039 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes an interferon analogue, whi and antitumor activity, and shows a synergistic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New interferon omega polypeptide derivs. - useful as antiviral and antitumour agents, and new DNA sequences and genes coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hauptmann
Pieler C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pieler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1985;
01-AUG-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BOEH ) BOEHRINGER INGELHEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP170204-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interferon-omega; virucide; antitumor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferon-pseudo-omega-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1986-036962/06
                                                                                                                                                              ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . R,
Hauel
    activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 14; 115pp; German.
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meindl P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85DE-3505060.
84DE-3428370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= interferon-pseudo-omega-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2951..3251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%;
  chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dworkin-Rastl E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                             ВP
inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7
0.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which has virucide tic increase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other
                                            bowel disease;
                                                                                         thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                  ARDS;
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Qy

149 GGCCCTGGTGGCATGGGCTCAC 170

GGCCCTGGTGGCATGGGCTCAC 123524

Matches Query Match

Local

22; Conser

100.0%;

Score 22; Pred. No.

DB 24;

Length 147724;

0;

Mismatches

0

0;

Gaps

0,

Db 123545

RESULT

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chronic) in a tissue, an allergic response in a subject exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation disease (e.g., precially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile
                                                                                                                                                                                                        inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease using the subject to a pathogen or sterile inflammatory disease using the
                                                                                                                  parasitic infection, protozoal infection, fungal infection and M5 useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocyte Note: The sequence data for this patent did not form part
       Sequence 147724 BP;
                                                                          of the printed specification, but was format directly from WIPO at
                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                            parasitic infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression profile; (3) detecting (M4) an inflammation (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identif DNA chip analysis as given in the specification, and comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2000; 2000US-237189P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID No 137;
  46968 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114pp; English.
  29251 C; 28325 G;
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                                                                                              obtained
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                                                                                                nT
43180 T; 0 other;
                                                                                              electronic
                                                                                                                                          granulocytes
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AAS91061/c
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                                        Вþ
                                                                                                                            Matches
                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 26865; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess high contents of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #26865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                              Sequence 1179 BP; 348 A; 292 C; 315 G;
                                        284
                                                                                 191 GGGTTGCAAAGATCTGTGGG 210
                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-639362/73.
DB; ABG26874.
                                        GGGTTGCAAAGATCTGTGGG 265
                                                                                                                              20;
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0540217
2000US-0649167
                                                                                                                                              5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                              Score 20; pred. No.
                                                                                                                            0;
                                                                                                                              Mismatches
                                                                                                                                                                                                                224 T; 0 other;
                                                                                                                                              DB 23; Length 1179; 6.7;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forensic;
                                                                                                                              0,
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                                                                                                                              Gaps
                                                                                                                              0;
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RESULT 9
AAC90702/c
                                                                                                                                                                         Matches
                                                                                                                                                                                              Query Match
Best Local
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                                                                                        2377
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P-PSDB; ABG02487.
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                                                                                                                                                                                                                                                             Sequence
                                                                                                                              32
                                                                                                                                                                       . Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT,
                                                                                                                                                                                                                                                             2526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
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RESULT 8
AAS66674
ID AAS66674 standard; cDNA; 2526

ВP

AAC90702

AAC90702 standard; cDNA;

ВP

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, formatics, agene manning identification of mittations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 2478; 103pp; English.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                    TTTCATCTTTGCAGGGACTT 51
TTTCATCTTTGCAGGGACTT
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                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                       BP; 871 A; 536 C;
                                                                                                                                                                                      5.1%;
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2396
                                                                                                                                                 0;
                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                       541 G;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                       578 T; 0 other;
                                                                                                                                                                                      DB 2
6.6;
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                                                                                                                                                                                                                              Length 2526;
                                                                                                                                                         Indels
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14-MAR-2001

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RESULT 10
AAX849/C
ID AAX849
XX AAX849
XX AAX849
XX AAX849
DT 30-JUL
XX Human
XX Gevelo
KW Inmune
KW Cognitam
KW Cognitam
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemla; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC90701 to AAC90715 encode the human secretory proteins given in AAB36661 to AAB36675. The proteins can have cytostatic, anti-inflammatory, haematopoietic, anti-coagulant, immunomodulatory and hepatotropic activities, and can be used as cell migratory agents, cell proliferation stimulants and cell differentiation-inducers. The proteins are useful in the treatment and prevention of diseases such as cancer, lung function disorder, liver function disorder, gastrointestinal disorder and immune diseases. AAC90716 to AAC90755 represent PCR primers which are used in the exemplification of the present invention.
                                                                                                                                                                30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel secretory protein and its salt with e.g. anti-cancer, anti-inflammatory and hematopoietic, effects, applicable as remedies and preventives to treat diseases like cancer and
                                                                                                                               Human secreted protein gene No. 17.
                                                                                                                                                                                                                             AAX84949 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-2000; 2000WO-JP03221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secretory protein; cancer; immune disease; infectious lung function disorder; liver function disorder; antlinflamma gastrointestinal disorder; cytostatic; haematopoietic; anticommunomodulatory; hepatotropic; cell proliferation-stimulant;
                                                                                                                                                                                                                                                                                                                                          217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-1999;
                                                                                                                                                                                                                                                                                                             238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                          GTGGTTTCCTGGATGGGGT
                                                                                                                                                                                                                                                                                                          GTGGTTTCCTGGATGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-032023/04
DB; AAB36662.
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                                                                                                                                                                                                                                                                                                                                                                        19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                   366 BP;
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                             DNA;
                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 97 C;
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    4.88;
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                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                   83 G;
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                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              87 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 366; 21;
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                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anticoagulant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune
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RESULT 11
AAC68089/c
ID AAC680
XX
AC AAC680
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AC AAC680
XX
DT 20-FEB
XX
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX8493) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 125 novel genes and their fragments (nucleic acid sequences AAX84933-X85057; amino acid sequences AAY27567-Y27933) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 125 polynucleotides, based on which tissues they are most highly expressed in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 125 polynucleotides, based on which tissues they are most highly expressed in the content of the content of
                                                       AAC68089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human
disorders
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07-NOV-1997;
07-NOV-1997;
07-NOV-1997;
                                                                                          AAC68089
                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                          GTGGTTTCCTGGATGGGGT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-337740/28.
DB; AAY27583. .
                                                                                                                                                                                                                                                                                                                                                                          AAX84933
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                                                                                                                                                                                                                                                        19; Conservative
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1, Shi Y, S
                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                    802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 290; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins and coding sequences useful for treating of the immune system and hyperprofiles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ebner R,
                                                                                                                                                                                                                                                                                                                                  B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the immune system and hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                     for described uses).
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97US-0066095.
97US-0066089.
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97US-0064988
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97US-0064985.
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                                                                                                                                                                                                                                                                                                                                    208
                                                                                          cDNA;
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                                                                                          1982
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                                                                                                                                                                                                                                                                                                                                C; 190 G; 188 T;
                                                                                                                                                                                                                                                                            Score 19;
Pred. No.
                                                                                        ВP
                                                                                                                                                                                                                                                          Mismatches
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i J, Olsen HS,
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21;
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                                                                                                                                                                                                                                                                                                                                6 other;
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                                                                                                                                                                                                                                                                                           Length
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20-FEB-2001

(first entry)

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RESULT 12
ABL09112
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Matches
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                                                                                                                                                                                                                                                                                                                 proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antipagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of genes AAC68081-C68127 encoding 47 human secreted proteins AAB37348-B37394. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (AAC68072) for increasing the stability of the fusion protein as compared to the human protein only. The genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human secreted proteins, used to treat, ameliorate or diagnose conditions such as cancer, and autoimmur diseases e.g. arthritis - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein cDNA sequence #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological disease; infection; human; secreted
Drosophila melanogaster expressed polynucleotide
                              26-MAR-2002
                                                           ABL09112;
                                                                                      ABL09112 standard; cDNA; 2770
                                                                                                                                                                                                                                                                         Sequence 1982 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Pages 321-322; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611702/58
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(ROSE/) ROSEN C A.
                                                                                                                                                                                       326
                                                                                                                                                             860 TTTTCTTCATTCTCTGTGG
                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                      parasitic
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19; Conser
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                              (first entry)
                                                                                                                                                                                                                                                                                                         infections.
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99US-0171504.
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                                                                                                                                                                                                                               4.8%;
100.0%;
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                                                                                                                                                             842
                                                                                                                                                                                       344
                                                                                                                                                                                                                               Score 19;
; Pred. No.
                                                                                                                                                                                                                    0
                                                                                        BP.
                                                                                                                                                                                                                   red. No. 21;
Mismatches
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 SEQ
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   NO
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                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevent,
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                       RESULT 13
ABL28930/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                    1050 GGTCACACAATCACTCACT 1068
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2770 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions
 23-MAR-2000; 2000US-191637P
                              23-MAR-2001; 2001WO-US09231
                                                                                                                 Drosophila melanogaster
                                                                                                                                              pharmaceutical; gene;
                                                                                                                                                             Drosophila;
                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ
                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                 ABL28930;
                                                                                                                                                                                                                                                                            ABL28930 standard;
                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                               233 GGTCACACAATCACTCACT 251
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                            developmental biology; cell signalling; insecticide;
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ilarity 100.0%;
Conservative
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2000US-0614150
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                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   786 A; 625 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21818; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 19; DB
%; Pred. No. 20;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 G; 730 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2770;
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RESULT 14
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Best Local
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                               Detection of Addison's disease or persons - using a 21-hydroxylase peptide fragment associated with Addison's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
          Disclosure; Column 6;
                                                                                 WPI; 1995-043462/06
                                                                                                                                   (UYFL ) UNIV
                                                                                                                                                            24-MAY-1993;
                                                                                                                                                                                   24-MAY-1993;
                                                                                                                                                                                                                                   US5376533-A
                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                 human adrenal gland ci
Addison's disease; ss
                                                                                                                                                                                                                                                                                                                                 21-hydroxylase fragment A,
                                                                                                                                                                                                                                                                                                                                                         05-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          AAT45064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4902 BP; 1509 A; 1006 C; 984 G; 1403 T;
                                                                                                                                                                                                                                                                                                          Polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGGGCTTTTTTTTTGG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
19; Conserv
                                                                                                           NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 38263;
                                                                                                                                  FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                        Song YH,
                                                                                                                                                                                                                                                                                             iin reaction; primer; PCR; amplify; 21-hydroxylase gene;
gland cDNA library; diagnosis; detection;
                                                                                                                                                         93US-0066281
                                                                                                                                                                                  9308-0066281
                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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100.0%;
       9pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for elucidating ce
                                                                                                                                                                                                                                                                                                                                forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers
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                                          at risk from developing to detect autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nt for detecting 1000 or more cell signalling and cell-cell
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RESULT 15
AAZ43080/c
ID AAZ430
                       \begin{array}{c} \mathsf{C} & \mathsf
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Matches
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    This sequence encodes a Caenorhabditis elegans insulin-like protein, and can be used in the method of the invention. The method is for analysing an effect of expression or mis-expression of a C. elegans insulin-like gene, and comprises observing a first nematode genetically engineered to express or mis-express a C. elegans insulin-like protein (ILP) of any one of groups I, II or IV or a derivative or fragment that displays one or more functional activities of the C. elegans ILP. The insulin-like genes in C. elegans constitute very useful tools for probing the function and regulation of their corresponding pathways. This can be expected to lead to the discovery of new drug targets, therapeutic proteins, diagnostics and prognostics useful in the treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-1998;
08-MAY-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAT45064-75 are primers which were used to amplify fragments of the 21-hydroxylase gene from a human adrenal gland cDNA library. The amplified fragments encode peptides which were used in the method of the invention to diagnose or detect Addison's disease. Fragment A comprises amino acids 1-162, fragment B, amino acids 164-271, fragment C, amino acids 272-356, and fragment D, amino acids 164-271, fragment E, amino acids 272-356, and fragment F manino acids 197-298 of the 21-hydroxylase enzyme. These primers have been optimised for use and do not directly correspond to 21 hydroxylase gene sequences. All the forward primers contain BamHI sites and all the reverse primers contain EcoRI restriction sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 8; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-013239/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EXEL-) EXELIXIS PHARM INC.
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les 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans insulin-like gene proteins of the C. elegans insulin-like g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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98US-0074984.
98US-0084303.
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Pred. No.
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67;
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therapeutic
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CC and clinical problems associated with the function of insulin hormones in CC humans and other animals, as well as clinical problems associated with CC aging and senescence. The information may also be useful in CC identification and validation of pesticide targets in invertebrate pests CC that are components of these signalling pathways. The genes are also CC useful for identifying factors that are upstream of the receptor in the cC genes provide a superior approach for identifying factors that are Upstream of the receptor in the signal transduction pathway.

SQ Sequence 339 BP; 92 A; 86 C; 72 G; 89 T; 0 other;

Ouery Match
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

188 TGTGGGTTGCAAAGATCT 205
DD 260 TGTGGGTTGCAAAGATCT 243

Arch completed: April 25, 2003, 00:01:03
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AQ165256 HS_3025_B
AQ237815 RPCII1-70
AQ442274 HS_5137_A
AQ437684 HS_5137_A
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ALIGNMENTS

MEDLINE COMMENT VERSION KEYWORDS SOURCE RESULT 1 AQ770688 LOCUS REFERENCE ACCESSION DEFINITION TITLE ORGANISM JOURNAL AUTHORS 470 bp DNA linear GSS 28-JUL-:
HS_5368_B2_C08_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=944 Col=16 Row=F, DNA sequence.
AQ770688
AQ770688.1 GI:5648804
GSS. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 470)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,Y., Swartzell,S., Adams,M.D. a Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-ll. For BAC library availability, please contact Pieter de Jong High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seati Tel: (206) 616-3618 Fax: (206) 616-3887 99380589 Contact: Mahairas GG, Wallace JC, Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) human. Seattle, Hood WΑ 98109, 28-JUL-1999 and and

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                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood High Throughput Sequencing Center University of Mashington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618

Fax: (206) 616-3887
                                                                                                                                                                                                                                                                            Hood,L. Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                     Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3025 row: N column: 12
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 525)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ165256 DNA linear GSS 16-OCT-19: HS_3025_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=12 Row=N, DNA sequence.
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Class: BAC ends
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a 112 c 131 g 141 t 3 others
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/db_xref="taxon:9606"
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                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
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                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                          BAC ends.
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                                                         /db_xref="taxon:9606"
/clone="RPCI-11-70H4"
/clone_lib="RPCI-11"
                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:7526667"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" a 139 c 137 g 143 t 4 others
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
                                          /sex="Male"
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3025 Col-12 Row-N"
/clone_lib="CIT Approved Human Genomic Sperm Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:3670106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.9%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 146; DB 17;
Pred. No. 1.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                             Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
   Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                             MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
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BASE COUNT
ORIGIN
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AQ442274
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            Вþ
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                                                                                                                                 BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 GAGTATGTAAAACTCCTGGGTCTCTGTGTGCCTGAG 194
              160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAG 98
                                          74
                                       TCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCT 108
              TCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ442274 410 bp DNA linear HS_5137_A1_F12_SP6E RPCI-11 Human Male BAC Library genomic clone Plate=713 Col=23 Row-K, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic clone Plate=713
AQ442274
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contract Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High Throughput Sequencing Compiversity of Washington 401 Queen Anne Avenue North, Tel: (206) 616-3618

Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human
Proc. Natl. Acad. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 410)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                        Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                      http://www.htsc.washington.edu
Plate: 713 row: K column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T / DOOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ442274.1 GI:4553613
                                                                        Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 410
                                                                      larity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPCI11 Human Male BAC Library"
150 c 164 g 189 t
                                                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

111 c 111 g 107 t 1 others
                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="Plate=713 Col=23 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n genome
Sci. U.S.A. 96 (17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; I Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38;
Pred. No.
                                                                     Score 35; DB Pred. No. 6e-0; Mismatches
                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                      6e-05;
                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WA 98109,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear GSS 31-MAR-1999
BAC Library Homo sapiens
                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 628;
                                                                                                   Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holzman, T., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                        0;
                                                                        Gaps
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
AQ437684
LOCUS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                  RESULT 6
AQ390599/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                         Qy
                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                 SOURCE
                                             KEYWORDS
                                                           VERSION
                                                                           ACCESSION
                                                                                                       DEFINITION
                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                          Matches
                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                              163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Nat
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                          AQ390599
AQ390599.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan
                                             GSS
               Homo sapiens
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                      Similarity
                               numan
                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa;
                                                                                                                                                                                                                                                                        8.8%;
100.0%;
   Chordata;
                                                                                                                                                                                                                                                          0;
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74 TCCTGGGTCTCTGTGTGTGTGCCTGAGTGGCTGCTCT 108
                                                                                                                                                                                                                                                                                                              TCCTGGGTCTCTGTGTGCCTGAGTGGCTGCTCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ437684 453 bp DNA linear HS_5137_A2_H06_Sp6E RPCI-11 Human Male BAC Library genomic clone Plate=713 Col=12 Row=O, DNA sequence. AQ437684 AQ437684.1 GI:4549023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC Clones are derived from the human BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 713 row: 0 column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                             635
CITBI-E1-2544B15.TR CITBI-E1
DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 453
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 127 c 117 g 124 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=713 Col=12 Row=0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                North, Seattle, WA 98109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 (17), 9739-9744 (1999)
Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
5.8e-05;
                                                                                                                                                                    sapiens
                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library RPCI-11.
                                                                                                                                                                                                                                                                                                                                                                                                                     0,;
Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 453;
                                                                                                                                                                    genomic
                                                                                                                                                                      GSS 06-MAR-1999 clone 2544B15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams, M.D.
  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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RESULT 7
AQ321916
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                                                                                                                                                                     Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD:
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 412)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
               library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
                                                                                      Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                        Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                  Unpublished (1998)
Other_GSSs: RPCI11-101H18.TV
                                                                                                                                                                                                                                                                                    Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter, Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS
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RPCI11-101H18.TJ RPCI-11
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence
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Class: BAC ends.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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The Institute for Genomic Research
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Use of BAC End Sequences
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/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
144 c 172 g 127 t
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/sex="male"
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/db_xref="taxon:9606"
/clone="2544B15"
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E., Wible,C., de Jong,P. and Venter,J.C.
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sapiens genomic clone RPCI-11-101H18,
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thes 0;
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                                                                                                                                                                               High quality sequence stop: 529
Location/Qualifiers
                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                 (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                 Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11.
Clibrary availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                           401 Queen Anne Avenue
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
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HS_5137_B1_F08_T7 RPCI-11 Human
genomic clone Plate=8905 Col=15
                                                                                                                                                                                                                                                       http://www.htsc.washington.edu
Plate: 8905 row: L column: 1
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Mammalia; Eutheria,
1 (bases 1 to 529)
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Class: BAC
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             /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and
                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=8905 Col=15 Row=L"
                                                                          /sex="male"
                                                                                         /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
102 c 120 g 116 t
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/db_xref="taxon:9606"
/clone="RPCI-11-101H18"
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Pred. No.
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Center
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g,J., Zhao,S., Adams,M.D.
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                                                                                                       193
                                                                               GTTGCAAAGATCTGTGGGAGAAGTGTGGTTTCC
                                                                                                      GTTGCAAAGATCTGTGGGAGAAGTGTGGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Shaying Zhao, William Nien
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Primates; Catarrhini; F
1 (bases 1 to 378)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ479650
RPCI-11-269D19.TV RPCI-11
                                                                                                                                                                                                                                                                                                                                                                                          Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f. Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Dr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
AQ147593 471 bp DN HS_3065_B2_H08_MF CIT Approved Human
                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
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llarity 100.0%;
Conservative
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                        BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hbe@tigr.org
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1 147 c 121 g 117 t
                                                                                                                                                                                           /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
103 c 93 g 66 t
                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="RPCI-11-269D19"
                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:7603002"
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                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                              /clone_lib="RPCI-11"
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                                                                                                                                          Score 33;
Pred. No.
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sapiens
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
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VERSION
                                                                                                                                                                                                                                                                                                   RESULT 11
AQ320567/c
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ORGANISM
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                                                                                                       TITLE
JOURNAL
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                                                                                                                                             AUTHORS
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  Clones are derived
                                                                                                                                                                                                            human
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens genomic clone Plate=3065
AQ147593
AQ147593.1 GI:3538246
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Scattle, Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3065 row: P Column: 16
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 471.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                    9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                              Contact: Shaying Zhao, William Nierman, Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD ;
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 482)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Colden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                      AQ320567
AQ320567.1
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RPCI11-99N1.TV
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                     hbe@tigr.org
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E-Coli DH10B"
a 118 c 123 g 84 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CIT Approved Human Genomic Sperm Library
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3065 Col=16 Row=P"
                                                                                                                                                                                                                                                                                                                                                                         GI:4050696
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Furlong,J., Young,J., Zhao,S., Adams,M.D.
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RPCI-11-99N1, DNA
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RESULT 12
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-NN1209-
151200-012-f04&t3=2000-12-15&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.K., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C. V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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PM4-NN1209-151200-012-f04 NN1209 Homo sapiens cDNA,
BF962702
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                                                                                                           quality sequence start: 15 quality sequence stop: 545. Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1209"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Gell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
121 c 106 g 112 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="RPCI-11-99N1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism≔"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No.
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. 0.00044;
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                                                                                                                                                                                                                                                                                                                                                                                       Sao Paulo-SP
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53 TGGGGCCGGAGTATGTAAAACTCCTGGGTCTCT 85

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BASE COUNT
ORIGIN
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KEYWORDS
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     Matches
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGCAAAGATCTGTGGGAGAAGTGTGGTTTCC
   33; Conserv
                                                                                                                                                                                                                                                                                                               Email: bb@@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other_GSSs: RPCI-11-185J19.TV
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RPCI-11-185J19.TJ RPCI-11 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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   Conservative
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                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
a 127 c 114 g 149 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                /db_xref="taxon:9606"
/clone="RPCI-11-185J19"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:7570890"
                                                                                                                                                                     /sex≖"Male"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                   100.0%;
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                   Pred. No. 0.0004
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Pred. No.
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library RPCI-11
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. 0.00042;
                 0.00042;
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                                  Length 563;
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                                                                                                                            EcoRI; Site_2:
 Indels
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333

TGGGGCCGGAGTATGTAAAACTCCTGGGTCTCT 301

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KEYWORDS
SOURCE
ORGANISM
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AQ386439/c
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AZ516454/c
                                                                        SOURCE
ORGANISM
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 GTTGCAAAGATCTGTGGGAGAAGTGTGGTTTCC 225
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                                                                                                                                                        DNA sequence.
AQ386439
AQ386439.1 GI:4357462
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Department of Eukaryctic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                  Eukaryota; Metazoa;
                                                                  Homo sapiens
                                                                                                                                           SSD
                                                                                                                                                                                                                                                             AQ386439 723
RPCI11-154D6.TJ RPCI-11 Homo
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Other_GSSs: RPCI-11-191D19.TJB
   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC end sequences of library RPCI-11 Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /GLUIC_____
/SEX="Male"
/SEX="Male"
/Cell_type="Lymphocytes"
/Cell_type="Lymphocytes"
/Cell_type="Lymphocytes"
/Cotle="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
/NOTE="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2: EcoRI; Site_2: EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:7573050"
/db_xref="taxon:9606"
/clone="RPCI-11-191D19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11"
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Chordata;
Primates;
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Pred. No.
                                                                                                                                                                                                                                                      723 bp DN
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
0.0004;
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                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are darilability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: RPCIll-154D6.TV
Contact: Shaying Zhao, William Ni
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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nao,S., Adams,M.D., Nierman,W., Malek,J.,
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ilarity 100.0%;
Conservative
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/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
165 c 135 g 199 t
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/clone="RPCI-11-154D6"
/clone_lib="RPCI-11"
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/db_xref="GDB:7558829"
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Pred. No.
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          Length DB
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       US-08-066-281-1
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US-09-452-239-3
US-09-452-239-3
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US-09-453-208-42
US-09-228-986-3
US-09-28-986-3
US-09-28-910-722-5
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US-08-487-033-17
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RESULT 2 US-09-397-787-254/c

Patent No.

254, App o. 646875

Application US/09397787

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APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
TITLE OF INVENTION: COMCER THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SEQ ID NOS: 334
SEQ ID NO 254
                                                                   US-09-452-239-3
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US-09-397-787-254
                                                                                                                                                                                                                                                                                 ; ORGANISM: Triticum aestivum US-09-452-239-37
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Matches 17
                Sequence 3, Application US/09452239 Patent No. 6465229 GENERAL INFORMATION:
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Patent No. 6465229
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Best Local :
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CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Rafalski, Antoni J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase FILE REFERENCE: BB1284 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cahoon, Rebecca E.
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                   LENGTH: 1118
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TYPE: DNA
ORGANISM: Homo sapien
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Query Match

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Score 17;

DB 4;

Length 1381;

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                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
File Reference: BB1284 US NA
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT APPLICATION NUMBER: 00/110,594
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/01
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Black, Micnael APPLICANT: Hodgson, John APPLICANT: Knowles, David APPLICANT: The Broke Brok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/858,207A FILING DATE: 09-MAY-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 709 Swederand
CITY: King of Prussia
                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                     TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity tes 17; Conserv
                                                                                             nucleic acid
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                                                                                                                                   1381 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SmithKline Beecham Corporation
709 Swedeland Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                 linear
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552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.3%;
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28;
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295 CATTTTTCTTCATTCTC 279 323 CATTTTTCTTCATTCTC Best Local Similarity Matches 17; Conserv

Conservative

339

100.08; ++

Pred. No. Mismatches

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Indels

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Gaps

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US-08-115-052-1

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Sequence 1, Application US/08115052 Patent No. 5705400
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1509 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                           FEATURE:
                                                                                                                                        FEATURE:
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 02-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                           NAME/KEY:
LOCATION:
                                                                                                                                                NAME/KEY: mat_peptide
LOCATION: 55..1494
OTHER INFORMATION: /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dale H. Hoscheit REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/937,409 FILING DATE: 31-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1509 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-5089299
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TISSUE TYPE: adrenal gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                          LOCATION:
                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 197430 BBMB UT
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misc_feature
                                                           misc_feature (435~436)
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13..54
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Assay for Adrenal Autoantigen
                             /standard_name= "PvuII cleavage
site"
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                                                          RESULT 8
US-09-453-702B-42/c
US-09-453-702B-42/c
; Sequence 42, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                 US-09-228-986-3
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: I
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Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 199-01-12
CURRENT FILING DATE: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
                                                                                                                                                                                                                                                                                                           LENGTH: 2686
TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CCATGCTGCTCCTGGGC 305
                                                                                                                                                                                                   318 TACCCCATTTTCTTCA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                       272 TACCCCATTTTTCTTCA 288
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LOCATION: (852~853)
OTHER INFORMATION: /sta
OTHER INFORMATION: site
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'ATURE:
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                                             APPLICANT: Blattner, Frederick R
                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 3.0
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Perna, N
Plunkett,
                              Burland,
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site"
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site"
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site"
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                 Nicole T.
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Pred. No.
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Pred. No.
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27;
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28;
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                                                                                                                                                                                                                                   Indels
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30-OCT-1996

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US-09-453-702B-42
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                                                                                                                                                                                                                                                      APPLICANT: Saxena, Richa APPLICANT: Hawkins Trevor APPLICANT: Reeve, Mary Pat TITLE OF INVENTION: DAZ: A G NUMBER OF SEQUENCES: 102 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        equence 102, Application US/08742185 stent No. 6020476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           )8-742-185-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2106 GGTTTCCTGGATGGGGT 2090
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                        STREET: Two Mills
CITY: Lexington
  APPLICATION NUMBER:
                                                                                                                                                         COUNTRY:
                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 17; Conserv
                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                           02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0
                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 11613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                 E: Hamilton, Brook, Smith & Reynolds, P.C Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                               David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
US/08/742,185
                                                                                                                                                                                                                                                                                             A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
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Pred. No.
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RESULT 10
US-08-910-722-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEFAX: (512) 474-7577
                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Roth, Jack A.
TITLE OF INVENTION: p16 EXPRESSION CONSTRUCTS AND THEIR
TITLE OF INVENTION: APPLICATION IN CANCER THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jin, Xiaomei APPLICANT: Roth, Jack P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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REFERENCE/DOCKET NUMBER: WHITELECOMMUNICATION INFORMATION.
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 GGTGGGGCTTTTTTTT 284
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patenth Release #1.0,
                                                  TELEFAX: (512)
TELEX: 79-0924
                                                                                                                   NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: IN
                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/910,722
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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TOPOLOGY: lir
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REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 31-JU
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5. 6251871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houston
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36 base pairs
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                                                                                                                                                                                                       08/502,881
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26;
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nucleic acid

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Best Local Similarity
Matches 16; Conserv
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Patent No. 6251871
GENERAL INFORMATION:
                                                         Matches
                                                                        Query Match
Best Local
                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INGN:016/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                           285 GGCTCCATGCTGCTCC 300
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ZIP: 77210
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29
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                                                                     Local Similarity
                                                                                                                              DESCRIPTION:
                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                     Highlander, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of
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                                                       ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arnold,
                                                                                                                                                             linear
                                                                                                                               other nucleic acid
/desc = "DNA"
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                                                                     Score 16; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                America
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                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
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93;
                                                                      DB 4; Length 42; 93;
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RESULT 12

RESULT 13

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US-08-474-177-17/c
                                                                                                                ; ORGANISM: US-08-474-177-17
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Patent No.
                                                          Matches
                                                                                    Query Match
                                                                         Best
                                                                                                                                                                                                                                                                             TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kamb, Alexander TITLE OF INVENTION: GERMLI
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APPLICATION NUMBER: 1
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CURRENT APPLICATION DATA:
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                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                              HYPOTHETICAL: I
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/227,369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/215,086
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                         MOLECULE TYPE:
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                 285 GGCTCCATGCTGCTCC 300
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                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 18-MAI
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50 GGCTCCATGCTGCTCC 35
                                                        Local Similarity
les 16; Conserv
                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                    nucleic acid
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1201 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                        larity 100.0%;
Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          linear
                                                                                                                                  Homo sapiens
                                                                                                                                                                               NO
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18-MAR-1994
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                                                                                       4.0%;
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                                                                                                                                                                                                                                                                                                                                                          28,957
                                                                                                                                                                                                                                                                                   17:
                                                                                                                                                                                                                                                                                                                                             24884-109348-E
                                                          0
                                                                        Score 16;
Pred. No.
                                                          Mismatches
                                                                         DB 1;
92;
                                                          0;
                                                                                    Length 57;
                                                          Indels
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RESULT 14
US-08-480-810-17/c
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US-08-487-033-17
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS
      Sequence
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: I
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 01 FILING DATE: 18-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
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PRIOR APPLICATION NUMBER: US 08/227,369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-MAR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                          285 GGCTCCATGCTGCTCC 300
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                                                                                                                                                      50 GGCTCCATGCTGCTCC 35
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17, Application US/08487033
o. 5739027
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16; Conserv
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Application US/08480810
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Db
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                            TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   MOLECUL: r
HYPOTHETICAL: r
                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-APR-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 18-MAR-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-MAR-1995 PRIOR APPLICATION DATA:
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810 TELEFAX: 202-962-8300
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                            285 GGCTCCATGCTGCTCC 300
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                                                             Local Similarity es 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1201 New CITY: Washington
                                                                                                                                       ORGANISM:
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GGCTCCATGCTGCTCC
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                                                             Conservative
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SYSTEM: PC-DOS/MS-DOS
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                         24884-109348
                                                             Mismatches
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92;
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                                                         Indels
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RESULT 15 US-08-508-735-17/c : Sequence 17, Application US/08508735 : Patent No. 5843756 : GENERAL INFORMATION:

0;

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APPLICANE: Stone, Steven
APPLICANE: Mand, ALAXANDAT
APPLICANE: Kamb, ALAXANDAT
APPLICANE: Kamb, ALAXANDAT
TITLE OF INVENTION: MYS GENE AND THERAPEUTIC USE THEREOF

ITHE MADRESSES: 47
CORRESONUENCE ADDRESS:
ADDRESSES: 47
CORRESPONUENCE ADDRESS:
ADDRESSES: Venable, Bactjer, Howard & Civiletti, ILP
STREET: 1201 New York Avenue, Suite 1000

ITH: Mashington
STREET: 20005
COMPUTER: IBE POPM.
MEDIUM TYPE: PLOPPY disk
COMPUTER: READABLE POPM.
MEDIUM TYPE: PLOPPY disk
COMPUTER: READABLE POPM.
MEDIUM TYPE: PLOPPY disk
COMPUTER: READABLE POPM.

COMPUTER: READABLE POPM.

MEDIUM TYPE: PLOPPY disk
COMPUTER: READABLE POPM.

SOFTWARE: PACHATION DATA:
COMPUTER: READABLE POPM.

APPLICATION NUMBER: US/09/508/735
CLINE DATE:
COMPUTER: READABLE POPM.

APPLICATION NUMBER: US/09/508/735
CLINE DATE:
COMPUTER: READABLE POPM.

APPLICATION NUMBER: 105
APPLICATION NUMBER: 28,957
APPLICATION NUMBER: 28,957
APPLICATION NUMBER: 29,957
APPLICATION NUMBER: 20,957
APPLICATION NUMBER: 2
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Title:
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Maximum DB seq length: 200000000
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5304.628 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Result

C ; No	- -	Score 33	Match 8.3	Match Length 8.3 684973	DB 10	ID US-09-263-959-1	Description
C	2	22	5.6	361	9	US-09-918-995-8549	Sequence 8549, Ap
O	ω	19	4.8	802	9	US-09-974-879-27	Sequence 27, Appl
C	4	18	4.5	430	10	US-09-876-889-254	Sequence 254, Ap
	ഗ	18	4 5	431	10	US-09-866-562-80	Sequence
	σ	18	4.5	431	10	US-09-866-562-87	Sequence
O	7	18	4.5	570	10	US-09-864-761-9118	Sequence 91
a	8	17	4.3	489	9	US-09-918-995-28049	Sequence 28049
O	φ	17	4.3	491	ø	US-09-918-995-34650	Sequence 34650
C L	0	17	4.3	492	9	US-09-918-995-19262	Sequence 19262
о Н	⊢	17	4.3	531	9	US-10-092-154-1899	Sequence 1899,
() 	2	17	4.3	531	10	US-09-764-847-1899	Sequence 1899
1	ω	17	4.3	553	10	US-09-864-761-13668	Sequence 13668, P
	4	17	4.3	609	10	US-09-974-300-8084	Sequence 8084,
c 1	5	17	4. 3	944	9	US-09-774-639-99	Sequence 99, Appl
ი 1	6	17	4.3	944	9	US-09-969-730-16	Sequence 16, Appl
_	7	17	4.3	1047	10	US-09-822-830A-468	Sequence 468, App
c 1	80	17	4.3	1089	10	US-09-962-740-3	Sequence
	9	17	4.3	1118	10	US-09-452-239-37	Sequence

Query Match

8.38,

Score 33;

DB 10;

		C	o		o		a		O		O							C			C	a	c	C
45	44	43	42	41	40	39	ა 8	37	36	35	34	<u>3</u>	32	31	30	29	28	27	26	25	24	23	22	21
16	16	16	16	16	16	16	16	16	16	16	16	17	17	17	17	17	17	17	17	17	17	17	17	17
4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3		4.3	4.3
321	281	255	238	121	121	121	121	121	121	121	121	1503841	1503841	1503841	326014	172637	38374	11613	2880	2686	1631	1396	1215	1215
10	10	10	10	9	9	9	9	9	9	9	9	10	10	9	10	10	10	9	٥		10	10	10	10
US-09-864-761-25530	US-09-964-824A-385	US-09-878-574-13480	US-09-878-574-5259	US-09-818-875-1334	US-09-818-875-1333	US-09-818-875-1330	US-09-818-875-1329	US-09-818-875-1326	us-09-818-875-1325	US-09-818-875-1322	US-09-818-875-1321	US-09-795-686-1	US-09-795-668-1	US-09-946-807-1	US-09-731-231A-3	US-09-805-458A-3	US-09-880-107-3463	US-10-114-170-42	US-09-951-502A-1	US-10-101-464A-3	US-09-962-740-5	US-09-962-740-8	US-09-962-740-6	US-09-962-740-1
Sequence 25530, A	Sequence 385, App	Sequence 13480, A	Sequence 5259, Ap	Sequence 1334, Ap	Sequence 1333, Ap	Sequence 1330, Ap	Sequence 1329, Ap	Sequence 1326, Ap	Sequence 1325, Ap	Sequence 1322, Ap	Sequence 1321, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3463; Ap	Sequence 42, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 5, Appli		Sequence 6, Appli	

ALIGNMENTS

US-09-263-959-1/c

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RESULT 1

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Sequence 1, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                                                          TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-199
CLASSIFICATION:
NAME: MCMASTERS, David D:
NAME: MCMASTERS, David D:
NAME: MCMASTERS, David D:
NAME: MCMASTERS, David D:
                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hood, Leroy E. APPLICANT: Rowen, Lee APPLICANT: Koop, Ben F.
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washing
                                                                                     TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Seed and Berry LLP STREET: 6300 Columbia Center,
                                                                TOPOLOGY:
                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98104-7092
                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                              684973 base pairs
                                                              linear
                                                                                                                                                                                                                        (206) 622-4900
                                                                                     single
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Length 684973;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; Homo sapiens US-09-918-995-8549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 404690 TGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAG 404658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8549
LENGTH: 361
TYPE: Now.
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Best Local Similarity 100.
"""" Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/09974879 Publication No. US20030028003A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: PCT/US98/23435
PRIOR FILING DATE: 1998-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PZ020P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 GGCCCTGGTGGCATGGGCTCAC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 TGTAAAACTCCTGGGTCTCTGTGTGTGTGCCTGAG
                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/064,912
FILING DATE: 1997-11-07
APPLICATION NUMBER: US 60/064,983
FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/064,911 FILING DATE: 1997-11-07
                                                         APPLICATION NUMBER: US 60/064,987
FILING DATE: 1997-11-07
APPLICATION NUMBER: US 60/064,908
FILING DATE: 1997-11-07
                                                                                                                                            APPLICATION NUMBER: US 60/064,988 FILING DATE: 1997-11-07
                                                                                                                                                                                      APPLICATION NUMBER: US 60/064,900 FILING DATE: 1997-11-07
                   APPLICATION NUMBER: US 60/064,984 FILING DATE: 1997-11-07
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 Human Secreted Proteins
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100.0%;
60/064,985
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; Pred. No. 0.0
0; Mismatches
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. 0.063;
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RESULT 5 US-09-866-562-80 ; Sequence 80, Application US/09866562

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; NAME/KEY: misc_feature
; LOCATION: (1)...(430)
; OTHER INFORMATION: n =
US-09-876-889-254
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PRIOR FILLING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,089
PRIOR FILLING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,095
PRIOR FILLING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,090
PRIOR FILLING DATE: 1997-11-17
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/876,889
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 353
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 254
LENGTH: 430
                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 254, Application US/09876889 Patent No. US20020076715A1
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS FILE REFERENCE: 210121.466C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Benson, Darin R. APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                               ORGANISM: Homo sapien FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/066,094
PRIOR FILING DATE: 1997-11-17
                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 802
                                 191 GGGTTGCAAAGATCTGTG 208
 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 GIGGITTCCIGGATGGGGT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 GTGGTTTCCTGGATGGGGT 235
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GGGTTGCAAAGATCTGTG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (359)
                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham, Jennifer L.
King, Gordon E.
                                                                     Conservative
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                                                                                      4.5%;
100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19;
Pred. No.
                                                                                                                                                         G
                                                                     Mismatches
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8.7;
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                                                                                                     Length 430
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INFORMATION:

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RESULT 7
US-09-864-761-9118/c
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                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 361,431
; OTHER INFORMATION: n = A,T,C or
US-09-866-562-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-866-562-87; Sequence 87, Application U; Patent No. US20020009758A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вb
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           Sequence 9118, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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Best Local
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APPLICANT: Penn,
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Switzer, Anne
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
FILE REFERENCE: 210121.502
CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Switzer, Anne TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER. FILE REFERENCE: 210121.502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Harlocker, Susan L. APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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NAME/KEY: misc_feature

LOCATION: 361,431

OTHER INFORMATION: n = A,T,C or G

09-866-562-80
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APPLICANT: Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                      UMBER OF SEQ ID NOS: 96
D ID NO 87
LENGTH: 431
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 431
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                             91 TGCCTGAGTGGCTGCTCT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; ples 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klee, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang, Tongtong
Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09866562
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Sharron G
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RESULT 8
US-09-918-995-28049/c
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
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Best Local S
Matches 18
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SOFTWARE: Annomax Sequence
SEQ ID NO 9118
LENGTH: 570
TYPE: DNA
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OTHER INFORMATION: E
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PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-05-26
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18; Conser
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                                                                                                                                                                                    Conservative
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N: EXPRESSED IN HELA, SIGNAL = 2.8

N: EXPRESSED IN PLACENTA, SIGNAL = 2.4

N: EXPRESSED IN BRAIN, SIGNAL = 4.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

N: EXPRESSED IN HEART, SIGNAL = 2.3

N: EXPRESSED IN LUNG, SIGNAL = 3.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1

N: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
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Pred. No.
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ADULT LIVER, SIGNAL = 4.4
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NAME/KEY: misc_feature; LOCATION: (1)...(491); OTHER INFORMATION: n = A,T,C US-09-918-995-34650
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Best Local Similarity
Matches 17; Conserve
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                                                                                   RESULT 10
US-09-918-995-19262/c
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LENGTH: 489
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34650
LENGTH: 491
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                                  GENERAL INFORMATION:
                                                 Sequence 19262, Application US/09918995 Publication No. US20030073623A1
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: HOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
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                 APPLICANT:
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LOCATION: (1)...(48)
[OTHER INFORMATION: n = A,T,C or
]9-918-995-28049
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                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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OF INVENTION: NO
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 NOVEL NUCLEIC ACID SEQUENCES OBTAINED
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Pred. No.
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US-10-092-154-1899/c
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US-09-764-847-1899/c
; ORGANISM: Homo sapiens
US-09-764-847-1899
                                                                                                                                                                                                                 Sequence 1899, Application US/09764847 Patent No. US20020132767A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1899
LENGTH: 531
TYPE: DNA
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19262
LENGTH: 492
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Best Local
                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1899
LENGTH: 531
TYPE: DNA
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009C1
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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                                                                                                Prior application data removed - NUMBER OF SEQ ID NOS: 2003
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ORGANISM: Homo sapiens
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LOCATION: (1)...(492)
OTHER INFORMATION: n = A,T,C
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; OTHER INFORMATION:
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US-09-864-761-13668
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US-09-864-761-13668/c
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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                                                                                                    FEATURE:
                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
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                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00667
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; OTHER INFORMATION: US-09-774-639-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-974-300-8084/c
Query Match
Best Local Similarity 100.0%; F
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8084
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/774,639 CURRENT FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 90 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 371
                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PZ013P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
                                                                                                                                           NAME/KEY: SITE LOCATION: (486) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 10085
                                                                                                           NAME/KEY: SITE
LOCATION: (934)
                                                                                                                                                                                       LOCATION: (13)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                        NAME/KEY: SITE
                                                                                                                                                                                                                                                        ORGANISM: Homo
                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                       LENGTH:
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les 17; Conserv
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                                                                                            equals a,t,g, or
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              Score 17; DB 9; Pred. No. 29; 0; Mismatches
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                                            Length 944;
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Command line parameters:

MODEL=frame+_p2n.model -DEV=x1h

-Q-cgn2_1/USPT0_spool_US09513999/runat_18042003_170936_28357/app_query.fasta_1.199
-De-cenemb1 -QFWT-fastap -SUFFIX=p2n.rge -MINNATCH=0.1 -LOOPCL=0 -LOOPEXY=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-USER=US09513999_@CGN_1_1_1687_@runat_18042003_170936_28357 -NCPU=6 -ICPU=3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XAAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
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score and is derived No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                                                  * NOTE: Estimated insert.size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Submitted (03-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 7, 2000 this sequence version replaced gi:8705345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Checko, J., Chen, Z., Cox, C. David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Dugan-Rocha, S., Durbin, K.J., Ganesh, R., Gorrell, J.H., Gorrell, Genesh, R., Gorrell, J.H., Gor
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Consensus quality: 139025 bases at least Q40
Consensus quality: 154842 bases at least Q30
Consensus quality: 154842 bases at least Q30
Consensus quality: 159725 bases at least Q20
Estimated insert size: 162720; sum-of-contigs estimation
Estimated insert size: 171608; agarose-fp estimation
Datimated insert size: 171608; agarose-fp estimation
Quality coverage: 3.9x in Q20 bases; agarose-fp estimation
Quality coverage: 4.1x in Q20 bases; sum-of-contigs estimation
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Center project name: HMQG
Center clone name: RP1-458H3
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                28690
28790
50833
50933
28689: contig of 28689 bp in
28789: gap of unknown length
50832: contig of 22043 bp in
50932: gap of unknown length
69144: contig of 18212 bp in
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Best Local Similarity:
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                                                                                                                                                                                                GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT 87331
                                                                                                                                                                                                                                                ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCCG 87382
                                                                                               sequence.
AC012378
AC012378.10
Rowen,L., Madan,A., Qin,S.; Baradarani,L., Burke,J., Dors,M., Fleetwood,P., Kaur,A.,
                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        1 (bases 1 to 199289)
                                                                                                                                    AC012378 199289 bp
Homo sapiens chromosome 15 clone
                                                                        Homo sapiens.
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/db_xref="taxon:9606"
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Submitted (09-AUG-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98105, USA
On Aug 9, 2001 this sequence version replaced gi:13775292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, I
Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-OCT-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Madan,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             center:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UWMSC]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owen, M.P., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 199289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 199289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: pUC18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://chroma.mbt.washington.edu/msg_www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: UWMSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Multimegabase Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-420M1"
/clone=lib="RPCI human bac library 11"
/clone_lib="RPCI human bac library 11"
/note="This clone overlaps CTD-2137J4 AC022083, RP11-458H3
AC012674 and RP11-291H24 AC009997. Data from overlapping
BACs were added and the consensus sequence determined from
RP11-420M1 to the extent possible."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="overlap with CTD-2137J4, AC022083"
49933. .50105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                               /note="overlap with RP11-291H24, AC009997"
40338 c 36951 g 58835 t
                                                                                                                                                                                                     /note="sequence data generated from subcloned PCR product"
72103. .72105
                                                                                                                                                                                                                                                    53940.
                                                                                                                                                                                                                                                                                       /note="low quality data"
53242. .53257
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                                                                                                                  166787.
                                                                                                                                                                                                                                                                                                                                                                                                     /note="low quality data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="low quality data"
52173. .52233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="15q21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="15"
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                                                                                                                /note="low quality data"
166787. .199289
                                                                                                                                                             55032
                                                                                                                                                                             /note="low quality data"
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                                                                                                                                                                                                                                                                                                                                          /note="low quality data"
52541. .52570
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="low quality data"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             James, R., Madan, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nesbitt, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloom, S.,
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VERSION
KEYWORDS
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                                                                                                                                                                                                                          FEATURES
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                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetGlyGlySerPheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyPro 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following absreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: LMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 15, 2001 this sequence version replaced gi:16605741.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human DNA
                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chrl
RPI1-424NL5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mamumalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Group.
                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                        VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                 sequence is the entire insert of clone RP11-424N15 The true t end of clone RP11-518L10 is at 64264 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Further information can be found
                                  18821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                       Location/Qualifiers
/note="Sequence from overlapping clone RP11-24C8
                                                      /clone_lib="RPCI-11.2"
                                                                                /clone="RP11-424N15"
                                                                                                          /chromosome="1"
                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152313 bp
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RESULT 4
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 CysValCysLeuSerGlyCysSer 36
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                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 161885 bases at least Q40
Consensus quality: 161940 bases at least Q30
Consensus quality: 162264 bases at least Q20
Consensus quality: 162264 bases at least Q20
Insert size: 166314; sum-of-contigs
Insert size: 164357; 4.9% error; agarose-fp
Quality coverage: 6.63x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 1
PROGRESS ***, 8 unordered
AL590557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requests: clonerequest@sanger.ac.uk
On May 8, 2001 this sequence version replaced g1:13990622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 163314)
                                                                                                                                                                                                                                                                                                  coverage: 6.67x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: bA24C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL590557.8 GI:13992136
                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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        1 16091: contig of 16091 bp in length
16092 16191: gap of 100 bp
16192 51184: contig of 34993 bp in length
51185 51284: gap of 100 bp
51285 67941: contig of 16657 bp in length
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ne 1 clone RP11-24C8,
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AL137847/c
                                                                                                         ACCESSION
VERSION
                                                                SOURCE
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                                                                                     KEYWORDS
                                                                                                                                                                       DEFINITION
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                  numan
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68042 10392
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fragment_chain:1"
68042 . .103921
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fragment_chain:1"
137192. .163314
/note="assembly_fragment:03121"
a 31325 c 32024 g 48050 t
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fragment_chain:1"
123849. .137091
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
51285. .67941
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/chromosome="1"
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fragment_chain:1"
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103921: contig of 35880 bp in length
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m clone RP11-439K3
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  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGTGCCTGAGTGGCTGCTCT 82259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATAGATTTCCTGCCTTGCCAGGGATCCTGGGGGCCAGAGTATGTAAAACTCCTGGGTCTC 82283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 http://www.sanger.ac.uk/HGP/Chr9 RP11-439K3 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
       148290 bp DNA linear PRI 01-JUL-2 Homo sapiens chromosome 15, clone CTD-3049M7, complete sequence. AC107979
AC107979.7 GI:21592043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt SWISSPROT}; \ {\tt Tr:}, \ {\tt TREMBL}; \ {\tt Wp:}, \ {\tt WORMPEP}; \ {\tt Information} \ {\tt on} \ {\tt the} \ {\tt WORMPEP} \ {\tt database} \ {\tt can} \ {\tt be} \ {\tt found} \ {\tt at} \ {\tt }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridgeshire, CB10 1SA,
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                                                                                                                                                                         Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 148290)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Chamarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Halme,W., Illev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Lind, G., Mardrean,C., Mardrean,C.
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                                                               Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Tot
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McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkty,L.,
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Birren, B., Linton, L., Nusbaum, C., Lander, E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nguyen, C., Nicol, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 26, 2002 this sequence version replaced gi:21321840. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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complement(1982. 2092)
/rpt_family="MIR"
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/rpt_family="MIR3"
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/rpt_family="Alusp"
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12818. .13060
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11229. .11338
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33366. .33524
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39530. .3
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29716. .2
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complement(26872. .26937)
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                                                                                                                          Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choppel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Mirohy, T., Marohy, G., Maylor,J., Meneus,L., Mihova,T., Mlenga,V., Michay, G., Maylor,J., Marohy, G., Marohy, 
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McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
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Birren, B., Nusbaum, C.,
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Direct Submission
Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 1, 2002 this sequence version replaced gi:21592191.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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1627. .16
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complement(1249. .19
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/rpt_family="L1PA13"
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14507. .15032
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5027. .5307
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7214. .7310
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23082. .23195
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18155. .1
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16450. .18
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/rpt_family="MIR"
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/rpt_family="MIR"
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19994. .20102
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23267. .23333
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20485. .20655
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Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rlse, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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* NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:21699255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 169861)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barran,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro C. Berreiga D. Bettellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC126324.2 GI:22123018
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                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L27749
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                                                                                                                                       Center project name: L27749
Center clone name: 358_H_20
                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center code: WIBR
                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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RESULT 9
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                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, M., Bastien, V., Boguslavki, L., Boukhgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Septers, M., Seaman, N., Steinen, R., Seaman, S., Severy, P., Seaman, S., Se
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AC090762.9
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192826 bp DNA linear PRI 28-FEB-:
Homo sapiens chromosome 15, clone RP11-387E8, complete sequence
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1 (bases 1 to 192826)
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1 71322: contig of 71322 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 192826)
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/clone_lib="RPCI-11 Human
33379 c 31394 g 49217
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/db_xref="taxon:9606"
/chromosome="11"
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                                Spencer, B., Stange-Thomann, N.,
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169861: contig of 98439 bp in length.
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Tesfaye, S., Theodore, J.,
                                Stojanovic, N.,
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5985
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5130
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4287
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Ferreira, P. FitzHugh, W., Gadega, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trajillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2002 this sequence version replaced gi:18377189. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 192826)
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------- Project Information
Center project name: L12392
Center clone name: 387_E_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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Center: Whitehead Institute/ MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1253
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                                                                                                                                                                                                                                                                                                                                                                                                        _family="THE1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="L1PB3"
                                                                               _family="AluJb"
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                                                                                                                                                                                                                                             _family="MIR"
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/rpt_ 12029

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/rpt_family_"LlMEc"
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24563. .24567
           /rpt_family="AT_rich" 32378. .32475
                                           /rpt_family="L1MB8"
31577. .31598
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complement(25258. .256
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/rpt_family="L1MEC"
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/rpt_family="MIR"
complement(15277..15553)
/rpt_family="MER8"
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/rpt_family="MIR"
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complement(8832. .8916)
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complement/10070
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complement/10/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(19978. 20262)
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16920. .16958
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                                                                                                                                                        family="Tigger2a"
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SOURCE
ORGANISM
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AC002421
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Best Local Similarity:
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JOURNAL
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                                                                                                                                                                                                                      AUTHORS
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                                                                 Submitted (12-AUG-1997) Center for Genetics in Medicine, the Washington University School of Medicine, 4566 Scott Avenuals, MO 63110, USA
On Jun 13, 2002 this sequence version replaced gi:2323248.
Current status of this project is available at:
'http://genome.wustl.edu/cgm/seq_projects.html'
Submitted by:
Ellson Chen,
Advanced Center for Genetic Technology,
Applied Biosystems Division of Perlin Elmer Corp.,
850 Lincoln Center Drive,
Foster City, CA 94404 USA
                                                                                                                                                                                                                 Unpublished (1997)
2 (bases 1 to 131347)
Brownstein, B.H., States, D.J. and Mazzarella, R.
                                                                                                                                                                                                                                                                                                                                                                                                                  AC002421
Homo sapiens chromosome X clone
***, 4 unordered pieces.
AC002421
AC002421.2 GI:21405641
                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 131347)
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                                                                                                                                                                     Medicine, Box 8232,
Scott Avenue, St.
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RESULT 11
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                                                                                                                                                                                                                                  TGTGTGTGCCTGAGCAGCTGCTTCT 103997
                                                                                                                                                                                                                                                                    CysValCysLeuSerGlyCysSerThr 37
                                                                                                                                                                                                                                                                                                         GATGGATCTGCCACCTTGCTGGGAATCCTGGGGCCAGAGTATGTAAAACTTCTGGGTCTC 103970
                                                                                                         sequence.
AL391375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e-mail: states@ibc.wustl.edu.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute for Biomedical Computing Washington University in St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David J. States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e-mail: buddy@genetics.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center for Genetics in Medicine, Washington University School of Medicine, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e-mail: ellson@genseq.apldbio.com
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REFERENCE
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only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats. Where the sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr: TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chapman, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/ChrX
RP11-375A20 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotated repeat sequence elements. Where the sequenambiguous, there is an annotation using the 'unsure'
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On Feb 2, 2001 this sequence version replaced gi:11414631
                                                                                                                          Homo sapiens chromosome
HTG; HTGS_PHASE0
                         AC126345.2 GI:22004319
                                                                AC126345
                                                                                             SEQUENCE SAMPLING
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/clone_lib="RPCI-11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hayoo, J., Kamat, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad Toh, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zembek,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 68314)
Birren, B., Nusbaum, C.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This record contains 84 individual
                                                                                                However, it should
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L27743
Center clone name: 100_E_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
Center project name: L27743
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,R., Vo,A., Wilson,B., Wu,X., Wyman,D.,
ek,L., Zimmer,A. and Zody,M.
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                                           be sequenced to completion.
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                                                                                           not be assumed that this clone
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me 11, clone RP11-100E23
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Grand-Pierre,N., Hagos,B.,
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14524: con''
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26816: contig of 727 bp 1
6916: gap of 100 bp
27618: contig of 702 bp 1
7718: gap of 100 bp
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9622: contig of 671 k
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530: contig of 709 bp i
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81 31780: gap of 100 bp
31 32509: contig of 729 bp 1
0 32609: gap of 100 hr
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32 33431 gap of 100 bp
34 153 contig of 722 bp
34 34253 gap of 100 bp
34 34253 gap of 711 bp
35 35064 gap of 100 bp
35 35064 gap of 695 bp
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100 bp

17 46436: gap of 100 bp

17 46436: contig of 692 b

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18 47228: gap of 100 bp

19 47951: contig of 723 b

100 bp
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43100: contig of 716 bp in length
43200: gap of 100 bp
43926: contig of 726 bp in length
44026: gap of 100 bp
44745: contig of 719 bp in length
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42384: gap of 100 hn
43100
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45552: contig of 707 bp
45652: gap of 100 bp
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153: gap of 100 k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratlovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Li, J., Li, Z., Lichtarge, O., Lieu, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nickerson, E., Nwekson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwekson, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwoon, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pilmus, E., Pu, L. L., Quiles, M., Ren, Y., Peters, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Sottk, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tanerisa, K., Tanerisa, K., Tanerisa, K., Tanerisa, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Walliams, G., Williamson, A., Wleczyk, E., Wooden, S., Worley, K., Wooden, S., Worley, K., Washington, C., Watlington, S., Pand, Gibbs, P., Elber, J., Rolfilla, S., Nelson, D., Washington, C., Walliamson, A., Wleczyk, E., Wooden, S., Welson, D., Washington, C., Walliamson, A., Wleczyk, E., Wooden, S., Welson, D., Washington, C., Walliamson, A., Wleczyk, E., Wooden, S., Welson, D., Washington, C., Walliamson, A., Wleczyk, E., Wooden, S., Wooden, S., Walliamson, A., Wleczyk, E., Wooden, S., Welson, D., Welso
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Esotto, M.,
Earlis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hayes, A., Hernandez, J.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Tacobson, R. Jia v. Tohoson, R., Jolivet, S., Joudah, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 143717)
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Baylor Plaza, Houston,
3 (bases 1 to 143717)
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On Apr 28, 200
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Direct Submission
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Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apr 28, 2002 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 143717)
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 19% of reads
Chemistry: Dye-terminator Big Dye: 81% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                                                          Center project name: HBNX
Center clone name: RP11-757N13
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                  Project Information
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BASE COUNT
ORIGIN
                                                                                 US-09-513-999C-7869_COPY_1_37 (1-37) x AC069245 (1-143717)
                                                                                                                                                                                                  Alignment Scores:
                                                                                                                            Query Match:
                                                                                                                                          Best Local Similarity:
                                                                                                                                                         Percent Similarity:
                                                                                                                                                                         score:
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                          34404 GATGGATTTCCCACCTTGCTGGGTATCCTGGGACCAGAGTATGTAAAACTCATGGGTCTC 34463
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CysValCysLeuSerGlyCysSer 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 16, 2000 this sequence version replaced 91:7249022. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently 
* consists of 17 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
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AC016472
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1. (bases 1 to 152354)
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Homo sapiens clone RP11-20P1, WORKING DRAFT SEQUENCE,
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                                                                                             be preserved
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Center clone name: 20_P_1
Center clone name: 20_P_1
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
0.0764525993883792Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 153000; agarose-fp
Insert size: 150754; sum-of-contigs
Quality coverage: 4.1 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.960731
Consensus quality: 142312 bases at least Q40
Consensus quality: 147429 bases at least Q30
Consensus quality: 149461 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
------    Project Information
                                                                                                                                                                                                                                                                                                                                                                      Quality c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44470 53277: contig of 8808 bp in length 53278 53378; gap of 100 bp 53378 71089: contig of 17712 bp in length 71090 71189: gap of 100 bp 71190 90983: contig of 19794 bp in length 90984 91083: gap of 100 bp 91084 112306: contig of 21223 bp in length 112307 112406: gap of 100 bp 112307 112406: gap of 100 bp 112307 112407 152354: contig of 39948 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44370 44469: gap of 100 bp
44370 53277: con+*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9207 9306: contig of 2376 bp in length
9207 9306: gap of 100 bp
9307 12163: contig of 2857 bp in length
9264 12263: gap of 100 bp
9264 15381: contig of 3118 bp in length
982 15481: gap of 100 bp
982 20100: contig of 4619 bp in length
11 23885: contig
6 23905
                                 /note="assembly_fragment"
91084. .112306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
6831. .9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="3810...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 27226: contig of 3241 bp

36 27226: gap of 100 bp

27 27326: gap of 100 bp

27 27326: gap of 100 bp

27 27326: gap of 3934 bp

28 36903: contig of 3934 bp

29 36903: gap of 100 bp
                                                                                                       /note="assembly_fragment" 53378. .71089
                                                                                                                                                                                       vector_side:right"
                                                                                                                                                                                                              clone_end:SP6
                                                                                                                                                                                                                                              /note="assembly_fragment"
32970. .36903
                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
20201. .23885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-20P1"
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44470. .53277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
 /note="assembly_fragment"
112407. .152354
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6730: contig of 2921 bp in length
6830: gap of
9206: contig of 500 bp
                                                                                    note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                         'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23985: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6730
                                                                                                                                                                                                                                                                                                                                                                                                                              .15381
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                                                                                                                                                                              .44369
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f 3241 t
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ACCESSION
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AC027295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117786 GATGGATTTCCCACCTTGCTGGGTATCCTGGGACCAGAGTATGTAAAACTCATGGGTCTC 117845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguuto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Hollows, S., Tondah, S.
                                                                                                                                                                                                                    Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mel, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokankwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ran, Y.,
Rives, M., Rojas, A., Rojubokan, T., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sutton, A., Syare, A., Tandr, H.,
Sutton, A., Syare, A., Tandr, H.,
Tandr, J., A.,
Tandr, J., Tandr, J.,
Tandr, J., A.,
Tandr, J.,
Tandr, J., A.,
Tandr, J.,
Tandr, J., A.,
Tandr, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspSerPheSerSerLeuGlnGlyLeuLeuGlyProGluTyrValLysLeuLeuGlyLeu
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Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,S. Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.J
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 160066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160066 bp DNA linear HTG 18-JUN-2002
Homo sapiens chromosome 12 clone RP11-293C20, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
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30395 c 30652 g 46711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
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REFERENCE
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FEATURES
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
Direct Submission
Submitted (30-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 160066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., weinstock,G. and Gibbs,R. Direct Submission Unpublished to 160066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc.helpebcm.tmc.edu
Contact: hgsc.helpebcm.tmc.edu
Contact: hgsc.helpebcm.tmc.edu
Contact: hgsc.helpebcm.tmc.edu
Contact: hgsc.helpebcm.tmc.edu
Conter clone name: HATS
Center clone name: HATS
Center clone name: HATS
Center clone name: BP11-293C20
Center clone name: BP11-293C20

Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 42% of reads
Chemistry: Dye-terminator Big Dye: 58% of reads
Chemistry: Dye-terminator Big Dye: 58% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 144209 bases at least Q40
Consensus quality: 149815 bases at least Q30
Consensus quality: 149815 bases at least Q30
Consensus quality: 153559 bases at least Q30
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/senbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
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contig of 9838 bp in length
gap of unknown length
contig of 15176 bp in length
contig of unknown length
contig of 20019 bp in length
gap of unknown length
contig of 20019 bp in length
gap of unknown length
contig of 25939 bp in length
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                                 29 CysValCysLeuSerGlyCysSer 36
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|49932 TGTATGTGCCTGAGCAGATGCTCT 49955
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47149 a 32911 c 32401 g 46353 t
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COMMENT

completed: April 24, ne : 1526 secs

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Command line parameters:

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-O-/cgn2_1/USPTO_spool/US9513999/runat_18042003_170936_28347/app_query.fasta_1.199
-DB-N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER=-US09513999_@CGN_1_1_200_@runat_18042003_170936_28347 -NCPU=6 -ICPU=3
-NO_XLDXY -NO_MMA.P -LARGEQUERY -NEG_SCORES=0 -WALT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=7
-NARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score 58.5 58 57.5 57 57 60.5 60.5 59 % Query Match 100.0 100.0 49.2 45.9 45.9 45.9 45.9 45.9 Length DB ID AAS69828 AAL16101 AAL16101 AAL24945 AAA223897 AA223897 ABA6320 ABA6320 AAC84220 ABA6320 AAC84220 AAC84220 AAC84220 AAC84220 AAC84220 AAC84201368 AAC84201362 AAC84201362 AAI18447 AAI43563 ABS11680 AAC80089 AAS91827 ABN25478 AAS88434 AAH98980 AAF658888 AAC03794 AAZ42680 ABK83461 ABA63453 ABA30652 AAK11985 ABQ56543 AAS64519 AAK53271 ABK73394 AAV49653 ABV05218 ABV14387 ABV35471 AAH57417 AAX87925 ABL32342 AAS68019 **AAK37688** AAI60469 SUMMARIES Murine LOBO genomi Murine LOBO homolo Human foetal liver Human foetal liver Human EXCS encodin DNA encoding novel Human nervous syst Human breast cance Human breast cance Description DNA encoding novel Human polynucleoti Bacillus lichenifo Human prostate exp Human prostate exp Human prostate exp Drosophila melanog Nucleobase permeas Chicken heparanase DNA encoding novel Human prostate exp Human immune/haema Novel human polynu Human immune syste DNA encoding novel DNA encoding novel Human EST-derived DNA encoding novel Human ORFX polynuc Probe #12249 used Human genome-deriv Probe Human cDNA differe Human Human Human Human secreted Human secreted stomach cell colon cancer SC1 DNA. bone marrow brain expres #9118 for ge #8380 for ge foetal immune/haema

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EN Huma
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C5-5
                                                                 Human; 5' EST;
gene therapy;
                                                                                                     Human secreted protein 5' EST,
                                                                                                                                                                         AAC03794 standard; cDNA;
                                                                                                                            06-OCT-2000 (first entry)
                        EP1033401-A2
                                             Homo sapiens
                                                                              5' EST;
                                                                 : expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
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                                                                                                     SEQ ID NO:
                                                                                                      3792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An arms encoding secreted proteins are sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping proc
21-OCT-1999
                           WO9953051-A2
                                                                                                                                                    Human
                                                                                                                                                                               01-FEB-2000
                                                                                                                                                                                                                                    AAZ42680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                     Homo
                                                                               regulation; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 447
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                                                                                    n; 5' EST; expressed sequence tag; secreted protein; diagnosis; therapy; chromosome mapping; upstream regulatory sequence; nsic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                     sapiens
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cregions (UTRS) and upstream regulatory regions which control the Coation, development stage, rate, and quantity of protein synthesis, as Coation, development stage, rate, and quantity of protein synthesis, as Coation, development stage, rate, and quantity of protein synthesis, as Coation, development stage, rate, and quantity of protein synthesis, as Coation and to deal as stability of mRNA. The ESTs are also useful as probes for Coations and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in Coations abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be consistent of a polypeptide or the Coation sertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have Coations and the identification of new secreted proteins is coation and the identification of new secreted proteins is coation.
Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis.
                                                                                                                                14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY65438 represent the EST-related proteins corresponding to AAZ42265 AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated
                                                                                             Human
                                                                                                                                                                   ABK83461;
                                                                                                                                                                                                      ABK83461 standard; cDNA; 128600
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28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                               1 MetGlyGlySerPheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyPro
                                                                                                                                                                                                                                                                        GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT
                                                                                                                                                                                                                                                                                                                                              ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGGCCG
                                                                                               CDNA
                                                                                        differentially expressed in granulocytic cells #32
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                                                                                                                              (first entry)
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98US-0069047
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Also included are modulating (MZ) GA by contacting GC with an agent
that alters the expression of at least one gene in Gs; (2) screening (M3)
for an agent capable of modulating GCA or an inflammation (especially
chronic) in a tissue, an altergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease using the
gene expression profile; (3) detecting (M4) an inflammation (especially
chronic) in a tissue, an altergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease, by detecting the
level of expression in a sample of the tissue of gene(s) from Gs, where
the level of expression of a sample of the tissue of gene(s) inflammation;

(A1) treating (MS) an inflammation (associative of inflammation;
                                                                                                                                                                                                                                                               glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, protozoal infection, fingal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                            (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, inflammation thrombosis cardiac response in a subject to a pathogen or sterile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel districts and inflammatory bowel districts of the disease; uncerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                            of the printed specification, but was format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA chip analysis as given in the specification, the expression level to an expression level in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 32; 114pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC INC
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                                                                                                                                                       BP;
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                       Mismatches:
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US-09-513-999C-7869_COPY_1_37 (1-37) x ABA63453 (1-570)
                                    Query Match:
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26-MAY-2000; 2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #11758
                                                                                                                                                            Note: The sequence data for this patent did not form printed specification, but was obtained in electronic
                                                                                                                                                                                      fetal liver. The present probe of the invention.
                                                                                                                                                                                                 measuring and displaying gene expression in samples derived fro
fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                        measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting,
                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid
                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00669
                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                               WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                         SEQ ID NO 11758; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-024263.
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                                                                                                                         156 G; 91 T; 0 other;
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US-09-513-999C-7869_COPY_1_37 (1-37)
                                                                                                                                                                                    predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems. Cardiovascular disease, hypertension, cardiac arrhythmias and e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                   Sequence 570
                                                                                                                                                  Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                              measuring human gene expression in a sample derived from human heart. present sequence is one such probe. The probes may be used for
                                                                                                                                                                                                                                                                      The present invention relates
                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                               Single
                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                             congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA30652 standard;
                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
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                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                               exon nucleic
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                                                                                                                                                                                                                                                                                              SEQ
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                    BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312.
                                                                                                                                                                                                                                                                                              No 9118;
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                                                                                                                                                                                                                                                                                                                                                                             DK,
                        0.000408
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61.11%
58.33%
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                                                                                                                                                                                                                                                                      to single exon nucleic acid probes for
                                                                                                                   156
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                                                                                                                                                                                                                                                                                           English
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Matches:
Conservative:
Mismatches:
Indels:
ABA30652 (1-570)
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                                                                                                                                                   the printed from WIPO
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                   US-09-513-999C-7869_COPY_1_37 (1-37) x AAK11985 (1-570)
                                              Query Match:
                                                       Best Local Similarity:
                                                                  Percent Similarity:
                                                                                       Pred.
                                                                                               Alignment
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AAK11985/c
                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                   probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; Alzheimer's disease; multiple sclerosis;
epilepsy; cancer; ss.
                                                                                                                 Sequence 570
                                                                                                                                                                                            The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                           Single
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                   brains
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                                                                                      NO . .
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                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 7
AAK37688/c
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                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and mveloma who make the province of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 12245; 658pp + Sequence Listing;
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27-SEP-2000;
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                                                GAGTATGTAAAATTCCTGGGTCTTTGTGTGTGCCTGAGTGGCCGCTCT 482
                                                                                                                                                  ATGAATGGATCT---
                                                                                                                                                                                             MetGlyGlySerPheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyPro
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234685.
; 2000US-02346359.
; 2000US-0024263.
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ID AAII8447 standard; DNA; 570 BP
XX
AC AAII8447;
XX
DT 12-OCT-2001 (first entry)
XX
Probe #8380 for gene expressio
XX
Probe; human; microarray; gene
KW cervical cancer; ss.

XX
OS Homo sapiens.
XX
OS Homo sapiens.
XX
OS Homo 2001; 2001WO-US00670.
XX
OS Homo 2001; 2000US-0180312.
PR
04-FEB-2000; 2000US-0204263.
PR
03-AUG-2001; 2000US-0608408.
PR
30-JUN-2000; 2000US-0632366.
PR
30-JUN-2000; 2000US-0670.
PR
21-EET-2000; 2000US-0670.
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21-EET-20
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                       RESULT 9
AAI43563/c
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray, which can be used for measuring human gene expression sample derived from human cervical epithelial cells. By measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID No 8380; 487pp; English.
AAI43563 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression, the probes are therefore useful in grading
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                            ATGAATGGATCT - -
                                                                                                                                                                                                                                         MetGlyGlySerPheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one such probe. The SENPs are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                               0.000408
88.50
61.11%
58.33%
45.85%
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570 BP
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                                                                                                                                                                                                                                                                                            (1-37) \times
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Matches:
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                                                                                                                                                                                                               RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity: Match:
                 Human genome-derived single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing
                                                                                                                                                                ABS11680 standard;
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03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                               GluTyrValLysLeuLeuGlyLeuCysValCysLeuSerGlyCysSer 36
                                                                                                                                                                                                                                                                                                                                                                                     GAGTATGTAAAATTCCTGGGTCTTTGTGTGTGCCTGAGTGGCCGCTCT 482
                                                                                                                                                                                                                                                                                                                                                          ATGAATGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                  .(first entry)
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2000US-0207456
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61.11%
58.33%
45.85%
                                                                                                                                                                DNA;
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                                                                                                                                                              ВP
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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Matches:
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                                                                                                                                                                                                                                                                                                                                                       ---CCTGCCTTGCTGGGATTCCTTGGGCTG 530
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                 from lung SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570
21
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                   ID No 11671.
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mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to they assigning exons to a single exon probe, having a mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons each of the exons in the tissues and/or cell types indicates that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human: ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary ciliary dyskinesis; pulmonary hypertension;
           pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon
                                                                                                                                         expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
                                                                                                                                                                                                                                                 the exons should be assigned to a single gene; a peptide comprising of 12011 sequences, mentioned in the specification, or encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
                                                                                                 fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's dis
Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis,
                                                                                                                                                                                                                                  probes/open reading frames (ORF). The probes are used for gene
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03-AUG-2000;
                                                                             haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spatially-addressable set of single exon nucleic
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2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-0323687
2000US-234687P.
2000US-236359P.
2000US-236359P.
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          The invention relates to the isolation of genes AAC68081-C68127 encoding 47 human secreted proteins AAB37348-B37394. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (AAC68072) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical
                                                                                                                                                                                                                                                                               (HUMA-)
                                                                                                                                             Nucleic acids encoding human secreted pamellorate or diagnose conditions such diseases e.g. arthritis -
                                                                                                                Claim 1; Pages 321-322; 387pp; English
                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein cDNA sequence #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC68089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC68089 'standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 570 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 GAGTATGTAAAATTCCTGGGTCTTTGTGTGTGCCTGAGTGGCCGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetGlyGlySerPheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyPro
                                                                                                                                                                                                         2000-611702/58.
DB; AAB37356.
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ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                    Ruben
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                                                                                                                                                                                                                                                                                                                      99US-0126598.
99US-0171504.
                                                                                                                                                                                                                                                    ,MS
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88.50
61.11%
58.33%
45.85%
    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection;
                                                                                                                                                                                                                                                  Komatsoulis
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      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
   gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 G; 91 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CCTGCCTTGCTGGGATTCCTTGGGCTG 530
                                                                                                                                                                                                                                                 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                        proteins, used to treat, prevent, h as cancer, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
The genes
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AAS91827/c
ID AAS91827 s
XX
AC AAS91827;
XX
DT 13-FEB-20C
XX
DNA encodi
XX
Human; chr
KW Human; chr
KW food suppl
XX
Food suppl
XX
HOMO Sapie
XX
PF 30-MAR-200
XX
PF 30-MAR-200
XX
PF 31-MAR-200
XX
PF 31-MAR-200
XX
PF 32-AUG-200
XX
PF 23-AUG-200
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PF 23-AUG-200
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PF 23-AUG-200
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PF 23-AUG-200
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PF 1 Drmanac RT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
        The invention polypeptide (1
                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                        biodiversity
                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1096 CTGGGTCTCTGCACGTGCTCAAGCGGCTACTCT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1156 GCTTTGCAGGAGTTGCAGTTACTTTTGCTGGGAAACCCCAGGGCCGGAGTATGTAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #27631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1982 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 LeuGlyLeuCysValCysLeuSerGlyCysSer 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyProGluTyrValLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parasitic
                                                                                                                                                                                                   2001-639362/73.
DB; ABG27640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scores:
                                                                                                                                                                                                                                                              RT,
                                                                SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                            Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections.
lates to isolated polynucleotide (I) and sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 A; 513
                                                        27631; 103pp; English.
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88.00
67.74%
64.52%
45.60%
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                                                                                                                                                                                                                                                            Tang
                                                                                                                                                                                                                                                            TΥ
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Best Local Similarity:
g x a x b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN25478,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating imaging of sites expressing (II), (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1299
                                                                                                                                                                                                                                                      WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                      autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN25478 standard; cDNA; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match:
                                                                                         30-MAY-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX polynucleotide sequence SEQ ID NO:19433
Shimkets RA,
                                                                                                                                                             29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                           06-DEC-2001
                                         (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          856 CTGGAGTATGTAAAGCTCCCAGGTCTTTGTGCATGCCGGAGCAGCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    916 GGCGGCAGCGAGGCTCCCTTGCCTGAGTTGCAGCCACATTTGTTGGGGATCCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 ProGluTyrValLysLeuLeuGlyLeuCysValCysLeuSerGlyCysSer 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GlyGlySerPheAla-----LeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGly 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                       2000US-206132P
2000US-228716P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
Leach MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 A; 349 C;
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62.16%
56.76%
44.56%
                                                                                                                                                                                                                                                                                                                                                gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative: Mismatches: Indels:
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Sequence 240 BP;

64 A; 61 C;

61 G; 54 T; 0 other;

at ftp.wipo.int/pub/published_pct_sequences

Š В Ş

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useful for treating burns, incisions, ulcers, for treating osteopor bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. OREX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                      sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                  N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Tablin the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP09726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID 19433; 1037pp; English.
                                                                                                                                                                                                                              for treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Table
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밁 δõ Alignment Scores: US-09-513-999C-7869_COPY_1_37 (1-37) x ABN25478 (1-240) Query Match: Score: Pred. Best Local Similarity: Percent Similarity: No . . 150 CCCGAGTATCTAAAGCTCCTGGGGCTCTGTATATGCCTGAGTAGCTGCTCT 100 20 ProGluTyrValLysLeuLeuGlyLeuCysValCysLeuSerGlyCysSer 0.000455 85.00 94.12% 82.35% 44.04% Indels: Gaps: Conservative: Mismatches: Matches: 00 240 14 2 36

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RESULT 14
AAS88434/c
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                DNA encoding novel human diagnostic protein #24238
                                                                                                                                                      13-FEB-2002
                                                                                                                                                                            AAS88434;
                                                                                                                                                                                                 AAS88434 standard; cDNA; 1909
        30-MAR-2001; 2001WO-US08631.
                               11-OCT-2001
                                                     WO200175067-A2
                                                                                                                                                      (first entry)
                                                                                                             forensic;
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SS

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RESULT 15
AAH98980
ID AAH98
XX AAH98
AC AAH98
XC AAH98
XX 12-OC
DT 12-OC
XX Human
XX Human
KW toman
KW diagn
KW diagn
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving abstrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC art for wino intention, but was obtained in electronic format directly from WIPO at the print of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-513-999C-7869_COPY_1_37 (1-37) x AAS88434 (1-1909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 24238; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                     tomato; monkey; dog; sea urchin;
diagnostics; forensic test; gene
                                       Human; sheep; pig; co
                                                                                                                                                                                                                           AAH98980;
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23-AUG-2000;
                                                                                                                            Human
                                                                                                                                                                      12-OCT-2001
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                                                                                                                    EST-derived coding sequence
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2000US-0649167.
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gene therapy;
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83.00
60.61%
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43.01%
cow; fruit fly; yeast; hamster; macaque;
g; sea urchin; expressed sequence tag; ES;
sic test; gene mapping; genetic disorder;
therapy; nutrition; ss.
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Conservative:
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Search completed: April 24, Job time : 165 secs

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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Cao
                                                                                                                                                                                                                                     proteins from a variety of organisms, including human, dog, cat, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, urchin and tomato. These were derived from expressed sequence ta from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence
                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                               Claim 1; Page 694; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                            of the invention.
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                                           273 GCCTTGCCTGAGATGCCATCACCTTTCTTGGGGATCCTAAGGCTGGAGTATGTAAAGCTC
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CTGGGTCTCTGTATGTGCCTGAGC
             LeuGlyLeuCysValCysLeuSer
                                                         AlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyProGluTyrValLysLeu
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DB; AAM24321.
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2000US-0663870.
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2000US-0617746
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A, Zhang
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-MODEL-frame+_pln.model -DEV=xlh
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-O-/cgn2_1/USPTO_spool_US09513999/runat_18042003_170937_28370/app_query.fasta_1.199
-DB=EST -OpMT=fastap -SUFFIX=pln.rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=US09513999_@CGN_1_1_1456_@runat_18042003_170937_28370 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRBADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPDP=6 -FGAPEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AQ770688	RESULT 1
<pre>1 (bases 1 to 470) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	GSS.	AQ770688.1 GI:5648804	AQ770688	genomic clone Plate=944 Col=16 Row=F, DNA sequence.	HS_5368_B2_C08_SP6E RPCI-11 Human Male BAC Library Homo sapiens	AQ770688 470 bp DNA linear GSS 28-JUL-1999		

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KEYWORDS
SOURCE
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                                                                                                                                                                                                            sapiens genomic clone
AQ165256
AQ165256.1 GI:3563451
                                                                                                                                                                                                                                             AQ165256 DNA linear GSS 16-OCT-1998 HS_3025_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=12 Row=N, DNA sequence.
                    Sequence-tagged connectors: A sequence
                                                      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 944 row: F column: 16
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Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
  scanning the human
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__Natl. Acad. Sci. U.S.A. 96 (17),
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/clone_lib="RPCI-11 Human Male BAC Library"
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/db_xref="taxon:9606"
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                                                          Adams, M.D.
                                                                            Holzman, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGCGGATCTTTCGCCTTGCAGGAAATTATNTCATCTTTGCAGGGACTTCTGGGGCCG 125
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 864)
                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ739814 864 bp DNA linear GSS 16-JUL HS_5505_Al_A09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=17 Row=A, DNA sequence.
                                                                    401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                         High Throughput Sequencing University of Washington
                                                                                                                                                             Contact: Mahairas GG,
                                                                                                                                                                            99380589
                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 96 (17),
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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University of Washington
401 Queen Anne Avenue North, Seattle,
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E-Coli DH10B"
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                                               Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3109 row: B column: 11
Class: BAC ends
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                                                                                                                                                                       High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
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                                                                                                                                                                                                                                                                                                          Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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Class: BAC ends
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                                                                                                                    Queen Anne Avenue North, (206) 616-3618 (206) 616-3887
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quality sequence stop: 519
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Male blood DNA was isolated from one randomly ci
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/db_xref="taxon:9606"
/clone="plate=1081 Col=17 Row-A"
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                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                            Seq primer: T7
                                                                                                                                                                                                              Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 604 row: D column: 3
                                                                                                                                                                                                                                                                                                                                                                                                  Scanning the human genome Proc. Natl. Acad. Sci. U.S
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HS_5028_B1_B02_T7 RPCIl1 Human N
                                                                                                                                                                                                                                                                                       Tel: (206) 616-3618
Fax: (206) 616-3887
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        /cell_type="Lymphocytes"
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                                                                                                         /organism="Homo sapiens"
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E-Coli DH10B"
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                                                                                                                                           Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@ttgr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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/db_xref="taxon:9606"
/clone="RPCI-11-70H4"
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Clones are derived from the human BAC library RPCI-11. For BA
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or
Research Genet cs (info@resgen.com). BAC end search page:
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics The Institute for Genomic Research
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/db_xref="CDB:7612823"
/db_xref="taxon:9606"
/clone="RPCI-11-994M24"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphocytes"
/note="Vector: pBAC63.6; Site_1:
/note="Vector: pBAC63.6; Site_1:
/note="bBAC63.6; Site_1:
/note
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                                                                                                                 TGTGTGTCTGAATGGATGCTCT
                              AQ427698
CITBI-E1-2575E9
              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A.,
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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R.Site 2 : EcoRI.
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
160 c 156 g 130 t
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/db_xref="taxon:9598"
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       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 418)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                   ng75g10.s1
similar to
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Other_GSSs: CITHI-E1-2575E9.TF
CONTACT: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tumor Gene Index
                                                                                                 Homo sapiens
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                                                                                                                                                                                     sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org
Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C. Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map Building
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/note-"vector: pBeloBAC11; Site_1:
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a 157 c 171 g 201 t 1
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/db_xref="taxon:9606"
/clone="2575E9"
/clone_lib="CITBI-E1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 529 Std Error: 0.00
Sec primpr: -/Anil 6:.4
                                                                                                                                                     Mammalia; Eutheria; Cnordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 556)
                                                                                                                                                                                                                                                     GSS
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RPCI11-138P7.TV RPCI-11
              Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                   AQ384817
                                                               Unpublished (1997)
Other_GSSs: RPCI11-138P7.TJ
                                                                                                                                               Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
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127 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone="IMAGE:940674"
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/lab_host="DH10B"
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTTGAGTGGCTGCTCT
Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-MG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
AG179297
AG179297.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC and search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                              Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                           BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-051111.TJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes DNA, clone: RP43-051111.TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
141 c 142 g 121 t
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/db_xref="GDB:7552974"
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RESULT 13
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                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                        9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                       Contact: Shaying Zhao, William Nierman, Mark
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
2. Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ534396
RPCI-11-38013.TJ
                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
135 c 122 g 192 t 3 others
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/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Sushiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-026N23.T7.
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AG160901.1
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168 c 156 g 194 t
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-MG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes/egsc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 27, Appl Sequence 27, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl	22 22 22 22 22 23 25 25 25 25 25 25 25 25 25 25 25 25 25	128	Sequence 3, Appli Sequence 2, Appli Sequence 1, Appli Sequence 10, Appli Sequence 8, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli

ALIGNMENTS

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	ATTORNEY/AGENT INFORMATION:	
	APPLICATION NUMBER: US 60/000,788	٠
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	CLASSIFICATION: 435	٠.
	FILING DATE: 03-JUL-1996	٠. ٠
	APPLICATION DATA:	
.30	SOFTWARE: PatentIn Release #1.0, Version #1.30	٠.
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	COMPUTER: IBM PC compatible	٠. ٠
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	COMPUTER READARLE FORM:	
	ZID: 0/30/-110/	
	STATE: California	٠.
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	STREET: 901 California Avenue	٠.
	ADDRESSEE: DNAX Research Institute	٠.
	SS	٠.
	SEQUENCES:	٠.
	INVENTION:	٠.
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		٠.
	APPLICANT: McClanahan, Terrill K.	٠.
	APPLICANT: Bazan, J. Fernando	٠.
	APPLICANT: Guimaraes, M. Jorge	٠.
	GENERAL INFORMATION:	٠. ٠
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415-852-9196

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                                                  Pred. No.:
                                                                                              ; ORGANISM: Homo sapiens US-09-341-587-5
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                   Percent Similarity:
                                                             Alignment Scores:
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                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09341587 Patent No. 6346606
                                                                                                                                                                                       APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REPERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                    09-341-587-5
                                                                                                                             TYPE: DNA
                                                                                                                                          LENGTH: 7379
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LOCATION:
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STRANDEDNESS: single
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RESULT 3
US-09-032-523-6
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US-09-513-999C-7869_COPY_1_37 (1-37) x US-09-032-523-6 (1-2073)
                                              Query Match:
                                                              Percent Similarity:
Best Local Similarity:
                                                                                               Score:
                                                                                                               Pred. No.:
                                                                                                                             Alignment Scores:
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APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Weil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                          TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                               LIBRARY: FALL
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                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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STATE: CA
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                                                          US-09-513-999C-7869_COPY_1_37 (1-37) x US-08-456-647B-19 (1-3120)
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US-08-456-647B-19
                                                                                                            Query Match:
                                                                                                                         Percent Similarity:
Best Local Similarity:
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ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., Jo
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APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
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REFERENCE/DOCKET NUMBER: 07251
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LOCATION: 485..3047
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ENGTH:
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PatentIn Release #1.0, Version
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US-08-237-401A-19 ; Sequence 19, Application US/08237401A ; Patent No. 5837448
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; Sequence 1, Application US/08875944B
               US-08-875-944B-1/c
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
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                                                                                                                                 91 GGGAGCTGGGCTCTTCAAGACTCA---
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                                                                                              ValLysLeuLeuGlyLeuCysValCysLeuSer
                                                                                                                                               GlySerPheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyProGluTyr 22
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IBM PC compati
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6096542

GENERAL INFORMATION:

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US-09-116-049-3/c
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Best Local Similarity:
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Sequence
                                                                                                                                                                                                                                                                                                                                                                 Ignment Scores:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YOSHIDA, KOICHI
APPLICANT: HIGASHINO, Fumihiro
TITLE OF INVENTION: CANCER CONTROL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00016
FILING DATE: 09-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                            158 TCATCACTGTCTGGT 144
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                                                                                                                                                                                     278 GGCGGCTTCCTGCAGGACAGGGCCGGGTCTGTGCGGGGACTCTGGGGGCTCCTTCTTG 219
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/875,944B FILING DATE: 07-AUG-1997 CLASSIFICATION: 514
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CITY: Washington
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                                                                                         ValCysLeuSerGly 34
3, Application US/09116049A
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SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hung, Men-Chie
TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
FILE REFERENCE: UTSC:582
CURRENT APPLICATION NUMBER: US/09/116,049A
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                   TELEFAX: (512) 474-75 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 2410 base pair:
                                                  REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 10-JAN-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                          NAME: Wilson, Mark B. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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Alignment Scores: Pred. No.:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/780,835 FILING DATE: 10-JAN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                    SEQUENCE
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/303,268
FILING DATE: 30-Apr-1999
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                            NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      TOPOLOGY:
                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                       LENGTH: 2410 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
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                                                                                  DESCRIPTION: SEQ ID
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US-09-676-610B-24/c
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Best Local Similarity:
CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 24
                                                                                                                                                                Patent No. 6444465
GENERAL INFORMATION:
                                                                                                                                                                                                      Sequence 24, Application US/09676610B
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                                                                       APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION
FILE REFERENCE: RTS-0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/116,049A CURRENT FILING DATE: 1998-07-15 NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hung, Men-Chie TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS FILE REFERENCE: UTSC:582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
RESULT 13
US-09-526-993-3/c
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US-09-526-993-4/c
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zwaal, Richard
APPLICANT: Asaert, Wouter
APPLICANT: Roelens, Ingele
APPLICANT: Roelens, Ingele
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C.
FILE REFERENCE: B0192/7012/ERG/KA
CURRENT APPLICATION NUMBER: US/09/526,993
CURRENT FILING DATE: 2000-03-16
EARLIER APPLICATION NUMBER: U.K. 9906018.8
EARLIER FILING DATE: 1999-03-16
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LOCATION: (163400)...(163586)
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LOCATION: (156827)...
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                                                                                  LeuLeuGlyLeuCysValCysLeu 32
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Sequence 3, Application US/09526993

Patent No. 6465715 GENERAL INFORMATION: ç

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APPLICANT: Zwaal, Richard
APPLICANT: Asaert, Wouter
APPLICANT: Asaert, Wouter
APPLICANT: Bogens, Ingele
APPLICANT: Bogaert, Thierry
ITTLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS IN C.
FILE REFERENCE: BO192/7012/ERG/KA
CURRENT APPLICATION NUMBER: US/09/526,993
CURRENT FILING DATE: 2000-03-16
EARLIER APPLICATION NUMBER: U.K. 9906018.8
EARLIER APPLICATION NUMBER: U.K. 9906018.8
EARLIER FILING DATE: 1999-03-16
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US-07-778-890A-2/c
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; ORGANISM: Caenorhabditis Elegans
US-09-526-993-3
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Best Local Similarity:
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                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR9003105, PCT/FR/91/00184

FILING DATE: 12-MAR-1990,07-MAR-1991
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Diskette-5.25 inch,360Kb storage
COMPUTER: LBM PC/XT/AT or compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS version 2.2
SOFTWARE: KEDIT or any ASCII Text Editor
CURRENT APPLICATION UMBER: US/07/778,890A
FILING DATE: 19920103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2176 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: 1.REY-SENELONGE Arielle APPLICANT: 2.KOHEN Gilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 CTCTTGAATATTTGTCGATGTTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 TTTGAATTTCAAAACAGTTTCGTTTCAATCGAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 LeuLeuGlyLeuCysValCysLeu 32
                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                       NUCLEIC
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                2176 base pairs
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39.29%
27.72%
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Indels:
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Conservative:
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                                            US-09-513-999C-7869_COPY_1_37 (1-37) x US-09-526-993-2 (1-3224)
                                                                                            Query Match:
                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                            Score:
                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                                                                          ; TYPE: DNA ; ORGANISM: Caenorhabditis Elegans US-09-526-993-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-526-993-2/c
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Best Local Similarity:
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APPLICANT: Zwaal, Richard
APPLICANT: Asaert, Wouter
APPLICANT: Roelens, Ingele
APPLICANT: Bogaert, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09526993 Patent No. 6465715
                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF DNA OR PROTEINS FILE REFERENCE: B0192/7012/ERG/KA
CURRENT APPLICATION NUMBER: US/09/526,993
CURRENT FILING DATE: 2000-03-16
EARLIER APPLICATION NUMBER: U.K. 9906018.8
EARLIER FILING DATE: 1990-03-16
NUMBER OF SEO ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circuta
MOLECULE TYPE: cDNA
HYPOTHETICAL: yes
                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 TTGAATGATGTTTTTACACTCCGCAGGCGCGCAGTTTGACTCCAGAGTATCTTAGCTAC 107
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PheAlaLeuGlnAspSerPheSerSerLeuGlnGlyLeuLeuGlyProGluTyrValLys
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Qy 25 LeuLeuGlyLeuCysValCysLeu 32
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Db 1200 CTCTTGAATATTTGTCGATGTTTG 1177

Search completed: April 24, 2003, 23:20:43
Job time: 58 secs

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-Q=/cgn2_1/USPT0_spoo1/US09513999/runat_18042003_170939_28423/app_query.fasta_1.199
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCCALICN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=USOAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=USOAL -CUTFMT=TD -TO-grunat_18042003_170399_28423
-NCPU=6 -TCPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NUES_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model -DEV=xlh
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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                                                                                   //cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
//cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
//cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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and is derived by analysis of the total score distribution.

9 US-09-918-995-8153 (10 US-09-783-590-1450	10 US-09-864-761-9118	c 1 93 48.2 684973 10 US-09-263-959-1 S	
10	64-761-9118 Sequence 9118, Ap	:	Description

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sequence 22, Appl Sequence 22, Appl	ນ ນ	209	209	541	22, 4	e 541	10	e 541,	541,	22, 1	e 541,	ιл	22,	209,	ιn	541,	541,	22, 1	54	541,	e 541,	e 22,	e 541,	N	1,	101, 2	e 6467	quence 4049, F	8266 A	Sequence 11, Appl	e 15	quence 19,	equence 68!	8	10	e 5991	Sequence 1349, Ap	27 200	Sequence 31393, A Sequence 14866, A

ALIGNMENTS

RESULT 1 US-09-263-959-1/c

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Sequence 1, Application US/09263959 Patent No. US20020150891A1 GENERAL INFORMATION:
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH
NUMBER OF SEQUENCES: 1279
                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      STREET: 6300 Co
CITY: Seattle
STATE: Washing
                                       FILING DATE: 0 CLASSIFICATION:
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                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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98104-7092
McMasters, David D.
                                                                                                                                                                                                                                                                   Washington
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PRIOR FILING DATE: 2000-03-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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                                  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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CURRENT FILING DATE: 2001-05-23
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 684973 base pairs
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APPLICATION NUMBER: GB 24263.6
REILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8153
LENGTH: 428
TYPE: DNA
                                      Query Match:
                                                                      Percent Similarity:
Best Local Similarity:
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US-09-864-761-9118
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Publication No. US20030073623A1
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
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US-09-513-999C-7869_COPY_1_37 (1-37) x US-09-918-995-8153 (1-428)

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SEQ ID NO 1450
LENGTH: 412
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                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (269)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: misc feature
LOCATION: (274)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: misc feature
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LOCATION: (265)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (5)
OTHER INFORMATION: n equals
ONAME/KEY: misc feature
                                                                                      OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (339)
                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (258)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (266)
COTHER INFORMATION: n equals a,t,g,
OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature
                                                    OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature
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Ruben, Steven M
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US-09-864-761-31393
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Best Local Similarity:
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                                                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TIVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR EILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-09-27
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LOCATION: (406)
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APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
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Hanzel, David K.
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Query Match:
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US-09-864-761-14866
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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SEQ ID NO 31393
LENCTH: 162
TYPE: DNA
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR EILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR EPILICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION UNMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                        PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/0066/
FILING DATE: 2001-01-30
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EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

EXPRESSED IN ADULT LIVER, SIGNAL = 3.6

SMISSPROT HIT: P98161, EVALUE 3.00e+00

EST_HUMAN HIT: A1792950.1, EVALUE 6.00e-07

NT HIT: AL163210.2, EVALUE 4.00e-04
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OTHER INFORMATION: MAP TO AC017089.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
OTHER INFORMATION: EXPRESSED IN ADULT LIVER,
US-09-864-761-14866
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Query Match:
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US-09-965-528-27
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APPLICANT: TANG, Y
APPLICANT: YUE, He
APPLICANT: LAL, Pr
APPLICANT: BURFORD
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27,
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00663
            CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-05-19
                                                                                               TITLE OF INVENTION: EXTRACELLULAR SIGNALING FILE REFERENCE: PF-0701 USA
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ORGANISM: Homo sapiens
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: 60/144,270
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BANDMAN, Olga
BAUGHN, Mariah R.
AZIMZAI, Yalda
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                                                                                                                                         LU, Dyung Aina M. PATTERSON, Chandra
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RESULT 8
US-09-764-868-1349
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                  US-09-783-590-5991
                                  RESULT 9
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Best Local Similarity:
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t Local Similarity:
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SEQ ID NO 1349
LENGTH: 24533
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Sequence 5991, Application US/09783590
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 1999-10-04
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                                                                     14284
                                                                                                                                        14224 CTGGGCTGGGCTGTGGCCTTGCTAGCGCTCGTGGTGGCGCCCCAGGAGCTTTTGGGTCCT 14283
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ORGANISM: HOMO
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                                                                                       GluTyrValLysLeuLeuGlyLeuCysValCysLeuSerGlyCys 35
                                                                     GAG---ATGCAACTGCTTGGACTGTGCCGGGGGATAGATAGGCTGC 14325
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                                                                                    RESULT 10
US-09-930-218-10/c
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Best Local Similarity:
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SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 5991
LENGTH: 506
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GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William
                                 Patent No. US20020034810A1 GENERAL INFORMATION:
                                                                   Sequence 10, Application US/09930218
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OTHER INFORMATION: n equals a NAME/KEY: misc feature
LOCATION: (351)
OTHER INFORMATION: n equals a NAME/KEY: misc feature
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APPLICANT:
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APPLICANT: goldshmidt, APPLICANT: pecker, ir
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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pecker, iris
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: LENCTH: 1605
: TYPE: DNA
: ORGANISM: Gallus gallus
US-09-930-218-10
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Query Match:
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APPLICANT: Robison, Keith E.
APPLICANT: RObison, Keith E.
TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT FAPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09833381 Patent No. US20020132090A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: AVENA AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE TITLE OF INVENTION: HEPARANASE ACTIVITY
FILE REFERENCE: 01/22335
CURRENT APPLICATION NUMBER: US/09/930,218
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/666,390
PRIOR APPLICATION NUMBER: 09/666,390
PRIOR PRIOR APPLICATION NUMBER: 09/666,390
PRIOR PRIOR PRIOR DATE: 2000-09-20
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1155
TYPE: DNA
ORGANISM: Homo sapiens
09-833-381-8
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                                                                                                                                                535 GTAGGAGGCACCTATACCCTTGTACATGCCAAAAATGCCCTCGGTCCGAGCTGTCTGCAG 594
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655 TGT 657
                                                                        595 CAGAGCGTACAGTATCCCTCGGTACATGAGGCCCTTTGCCCTGTGCATCTGTGCGGCTGGT
                                        35 Cys 35
                                                                                                        15 GlnGlyLeuLeuGlyProGluTyrValLysLeuLeuGlyLeuCysValCysLeuSerGly 34
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                                                                                                                                                                                         1 MetGlyGlySerPheAlaLeuGlnAspSerPheSerSerLeu-----
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Matches:
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US-09-158-722-19
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RESULT 12
US-09-974-300-685
; Sequence 685, Application (
; Patent No. US20020146721A1
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SEQ ID NO 685
LENGTH: 1380
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APPLICANT: Berka, R
APPLICANT: Clausen
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
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                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/158,722
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CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 154
LENGTH: 302250
TYPE: DNA
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US-09-962-832-154
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US-09-513-999C-7869_COPY_1_37 (1-37) x US-09-962-832-154 (1-302250)
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Best Local Similarity:
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Patent No. US20020110821A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturities of INVENTION: Sets
FILE REFERENCE: 689290-74
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                               LeuGlnAspSerPheSerSerLeuGlnGlyLeu-----LeuGlyProGluTyrValLys 24
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Matches:
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Indels:
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Db 174195 TGTGTGGGGGTGTGTGTGTGTTTTGTGGGTGT 174227
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; ANTI-SENSE: 1
US-09-044-604-11
Search completed: April 24, Job time: 153 secs
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Best Local Similarity:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Probefor human ENDO-I"
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NAME: Montgomery, Ilene
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
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CORRESPONDENCE ADDRESS:
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LENGTH: 250 base pairs
                                                                                                                                                                                                                                                                                                                                                                 No . .
                                                                             131 AGAGTGTTAAAGTAGGGGCAATGTCTTTCGCTG
                                                                                                                                                     191 GGGAGTAGTTGGGGTGTAGAACAACCTTTTCAATCTCTACAAGGTGCTTTTTCCCCCACAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 30500 No. US200
CITY: Farmington Hills
STATE: Michigan
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                                                                                                              22 TyrvalLysLeuLeuGlyLeuCysValCysLeu 32
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SUMMARIES

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ALIGNMENTS

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AC012674/c
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                    AUTHORS
                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169620)
                                                                                                                 AC012674
AC012674_10 GI:9719580
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                             Homo sapiens chromosome 3 clone RP1-458H3, 18 unordered pieces.
                  Muzny, D.M.,
                                                                                                                                                                                                                  AC012674
   Bodota,B.,
                                                                                                          Homo sapiens.
, Adams, C., Bailey, M., Barbaria, Bouck, J., Bowie, S., Brooks, A.,
                                                                                                                                                                                                                169620 bp
Barbaria, J., Blankenburg, K., rooks, A., Buhay, C., Bunac, C.,
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David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J.,
Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
Tabor,P., Taylor,T., Vasquez,L., Vinson,R., VO,Q., Wahbah,M.,
Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
Worley,R., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-NOV-1999) Human Genome Sequencing Center, I of Molecular and Human Genetics, Baylor College of Medic: Baylor Plaza, Houston, TX 77030, USA on Aug 7, 2000 this sequence version replaced gi:8705345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 18 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329
Consensus quality: 139025 bases at least Q40
Consensus quality: 154842 bases at least Q30
Consensus quality: 159725 bases at least Q20
Estimated insert size: 162720; sum-of-contigs estimation
Estimated insert size: 171608; agarose-fp estimation
Ouality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: HMQG
Center clone name: RP1-458H3
-----Summary Statistics
                                                                                                                                                                              107262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code:
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COMMENT

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hes 111; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCG
             Center: Washington University Genome Center code: WUGSC
                                                                   9 <del>M</del>
                                                                                         Submitted (25-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                     Direct Submission
                                                                                                                                                                       Submitted (29-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                              2 (bases 1 to 199038)
Waterston, R.H.
                                                                                                                                                                                                                                                                 1 (bases 1 to 199038)
Waterston, R.H.
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ACI16565.3 GI:20304073
ACI16565.3 PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                HOMO Sapiens chromosome 4 clone RP11-1263C18, WORKING DRAFT SEQUENCE, 6 unordered pieces.
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                Waterston, R.H.
                                                                                                                                                             MO 63108,
                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone
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                                                                  ) 63108,
) Apr 25,
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                                                        USA
, 2002 this sequence version replaced g1:20128757
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/db_xref="taxon:9606"
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RESULT 3
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Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197086 bases at least Q40
Consensus quality: 197086 bases at least Q30
Consensus quality: 197234 bases at least Q20
Insert size: 202000; agarose-fp
Insert size: 198637; sum-of-contigs
Quality coverage: 10.82 in Q20 bases; sum-of-contigs
Quality coverage: 10.82 in Q20 bases; sum-of-contigs
                                                                                                                           GGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT 111
                                                                                                                                                                                         CTGGAAGGATTGCCACCTTGCCAGGGATCCTGGGGGCCGGAGTATGTAAAACGCCT 58696
                                                                                                                                                                                                                   CTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCT 77
                                                                                                       GGGTCTCTGTGTGGGCTGAGTGGCTGCTCTGCT 58662
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29922. .74050
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198086. .199038
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/db_xref="taxon:9606"
/chromosome="4"
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46319 c 46377 g 52290 t
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3383: gap of unknown length
12884: contig of 9501 bp in length
12984: gap of unknown length
29821: contig of 16837 bp in length
29921: gap of unknown length
74150: contig of 44129 bp in length
74150: gap of unknown length
197985: contig of 123835 bp in length
198085: gap of unknown length
199038: contig of 953 bp in length
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Pred. No. 7.1e~12;
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Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Lou
MO 63108, USA
5 (bases 1 to 130636)
Waterston, R.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Sep 18, 2001 this sequence version replaced gi:14916171.
                                                                                                                                                                                                                                                                                                                                                                         4 (bases 1 to Waterston, R.H.
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Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haglund, K., Kozlowicz, A., Elliott, G. and Boyer, E. The sequence of Homo sapiens BAC clone RP11-30H15 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) 99063792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130636)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens BAC clone RP11-30H15 from AC092586 AC016389 AC092586.2 GI:15638723
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Drafting Center: WIBR
                                                              Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC
                    Center project name: H_NH0030H15
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                                        Summary Statistics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:

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В δÃ

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donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org The RPCI-11 human BAC library was made from the blood of one male

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FEATURES
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The clone sequenced to the left is RP11-111J6, 2000 bp overlap.
Actual start of this clone is at base position 149730 of
RP11-11J6; actual end is at base position 130636 of RP11-30H15.
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Location/Qualifiers
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9315, .9354
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/db_xref="taxon:9606"
/chromosome="2"
                             /rpt_family="L2"
11300. .11740
                                                                                                                                                                                                                                                         /rpt_family="L2"
7974. 8173
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10513. .11009
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                                                                                                                                    61 GAGTATGTAAAACTCCTGGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTAC
  140040 bp DNA linear PRI 09-APR-
Homo sapiens chromosome 10 clone RP11-93L14, complete sequence.
AC022029
AC022029.7 GI:197744073
                                                                                                                                                                                                                                   Conservative
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22376. .22535
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18879. .1917=
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25160. .25330
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22587. .22900
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21976. .22293
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18193. .18704
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12895. .14288
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|4747. .15888
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4321. .14437
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19176. .20870
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                                                                                                                                                                                                                                                 Score 65.2; DB 9;
Pred. No. 2.5e-11;
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                                                                                                                       GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT 111
                                                                                                                                                             ATGTATGGACCTCCCGCCTTGACTGAGTTGTAGTCACCTTTGCCAGGGATCCTGTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JAN-2000) Genome Therapeutics Street, Waltham, MA 02453, USA
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On Mar 28, 2002 this sequence version replaced
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is the entire insert of clone RP11-93L14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Genome Therapeutics Corporation Center code: GTC
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                                                                                                                                                                                                                                                                                                                                      /clone="RP11-93L14"
/clone_lib="RPCI-11"
26787 c 24761 g /
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/db_xref="taxon:9606"
/chromosome="10"
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73.9%;
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Dye-terminator Big
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                                                                                                                                                                                                                                                                                Score 64.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPI1-81003 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RPI1-81003 is at 1 in this sequence. true left end of clone RP6-204F4 is at 147189 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jun 14, 2001 this sequence version replaced gi:14280423. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL355812 147288 bp DNA linear PRI 13-JUN-20 Human DNA sequence from clone RP11-81003 on chromosome Xq22.3-24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL355812.23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-81003 is from the library RPCI-11.3 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmalia; Eutheria; Pr
(bases 1 to 147288)
                                                                                                                                                                                     /note="L1M4 r
2649. 337
                                                                                                               /note="L1MEc 3882. 4044
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/note="L1M4 5401. .5663
                                       /note="LIME3A repeat: matches 5257. 4724 ...5174
                                                                                                                                                                                                                                     /note="AluJo repeat: matches 2002. .2645
                                                                                                                                                                                                                                                                                1757.
                                                                                                                                                                                                                                                                                                                        1381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .147288
                                                                                               3882. .4044
/note="L1ME3A repeat:
                                                                                                                                                                           2649. .3323
/note="L1MC4 repeat: matches
                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11.3"
                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-81003"
                                                                                                                                                                                                                                                                                                                                                                         /map="q22_3-24"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                               /note="AluJb repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1 repeat: matches 4404 .4413 of consensus" 20105 .20666 // 20105 .20866 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 20105 // 2
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17066 .17368
1706e "AluSx repeat: matches 1 .302 of consensus"
17369 .1759
/note="LIME1 repeat: matches 5010 .5224 of consensus"
17654 .19512
/note="LIMA1 repeat: matches 4389 .6262 of consensus"
19745 .20100
/note="LIMC2 repeat: matches 5470 .5826 of consensus"
20094 .20104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16278. .17065

//octe-"LIME1 repeat: matches 1666. .1777 of consensus"
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/note="34 copies 2 mer tt 66% conserved"

11917. .12078

/note="LLME2 repeat: matches 5989. .6155

12171. .13851
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/note="Charliela repeat: matches 6. .417 of conser /note="Charliela repeat: matches 6. .417 of conser /note="MER58 repeat: matches 1. .83 of consensus"
                                                                                                                                                                                                     /note="L1MEc repeat:
24895. .25759
                                                                                                                                                                                                                                                                                                                                                                               /note="L1M4 repeat:
24021. .24198
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13877. .14584
/note="LIMA4 repeat: matches 5516.
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/note="Charliela repeat: matches 404. .1196 of consensus"
                                                                                                                                                                                                                                                                                                                      'note="L1M4 repeat: matches 2459. .2637 of consensus"
24207. .24312
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1PA14 repeat: matches 6004. .6149 of consensus"
23421. .24030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1M4 repeat: matches 3293, .3703 of
23269, .23420
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22853. .23268
                                                        'note-"LlMA9 repeat:
                                                                                                                                                                                                                                                                                      'note="L1M4 repeat: matches -3. .103 of consensus"
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                                                                                         e="AluSx repeat:
                                                                                                                                                                    "L1MA9 repeat:
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  repeat:
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                                                        matches 5346. .5440 of consensus'
                                                                                                                                                                       matches 5440. .6304 of consensus'
                                                                                                                                                                                                                                matches 2291.
                                                                                                              matches 1. .301 of consensus"
  matches
  .4781 of consensus"
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  .354
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                61 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT
                                                                                          1 ATGGGTGGATCTTTTGCCTTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCG 60
GAGTATGTAAAGCTCCTGGGTCTCTGTGTGTGCCTGAGCAGCTGCTTTGCT
                                                                                                                                           Conservative
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36495...36721
/note="Tigger3(Golem) r
consensus"
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/note="LIMA9 repeat: matches 2349.

29486. .29729

/note="LIMD3 repeat: matches 7485.

29737. .30026
                                                                                                                                                                                                                                                                                   /note="L1M4 repeat: matches 3439. .4077 of consensus"
43654. .44154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1MA8 repeat:
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                                                                                                                                                                                                                                                                                                                                                     /note="L1M4 repeat: matches
41348. .42700
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1M4c repeat: matches 1608, 39501, .40086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1M4 repeat: matches 2110. .2695 of 37639. .37766
                                                                                                                                                                                                                             /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                 /note="L1ME2 repeat: matches 4128.
14155. .44465
                                                                                                                                                                                                                                                                                                                      /note="L1M4c repeat: matches 940. .2376 of consensus"
12986. .43636
                                                                                                                                                                                                                                                                                                                                                                                    /note="L1M4b repeat: matches -273. .334 of consensus"
10087. .40139
/note="L1M87 repeat: matches 5776. .5828 of consensus"
10136. .41315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluSg repeat: matches 1. .307 of consensus"
19288. .39456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1M4c repeat: matches 1768. .1603 of consensus"
38992. .39287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="MER65A repeat: matches 1. .445 of consensus"
18696. .38991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1MA8 repeat: matches 5204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1MB7 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1PB1 repeat: 31299. .31641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1M4 repeat: matches 2187.
30716. .31150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1M4 repeat: matches 2689. .2989 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1MB8 repeat: matches 2920.
                                                                                                                                                            58.2%;
73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .37632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .34500
                                                                                                                                         Score 64.6; DB Pred. No. 4e-11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 5564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 5814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 5696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 5960. .6149 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches
                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                     -5.
                                                                                                                                           29;
                                                                                                                                                                                                                                 .310 of consensus
                                                                                                                                                                                                                                                                                                                                                                       .1210 of consensus"
                                                                                                                                                                            Length 147288;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2831 of consensus"
                                                                                                                                                                                                                                                                 .4602 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1769 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5597 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5253 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3279 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6166 of
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 50721
                                  111
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Human DNA sequence AL591048

75270 bp DNA linear PRI sequence from clone RP11-612M16 on chromosome

PRI

6, complete

complete

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TITLE
                                                                                                                                         Query Match
                                                                                        Matches
                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
1 ATGGGTGGATCTTTTGCCAGGATTCTTTTTCATCTTTTGCAGGGACTTCTGGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL: Sw.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-612M16 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-206F19 is at 73271 in this sequence right end of clone RP11-82M9 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP11-612M16 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on Aug 10, 2001 this sequence version replaced gi:15020550. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either doubtle stranding unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISSPROT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-AUG-2001) Sanger Centre, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Almeida, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL591048
AL591048.7 GI:15147695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Sequence from reads derived from a single pUC confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="6"
/clone="RP11-612M16"
/clone_lib="RPCI-11.3"
33923. .34247
                                                                                                                                                                                                                      confirm the assembly.

14850 c 13893 g 2
                                                                                                                                                                                                                                                                                                                                   confirm the assembly. 49353. .49464
                                                                                                                                                                                                                                                                                                                                                             /note="Sequence from reads
derived from a single pUC
confirm the assembly."
                                                                                                                                                                                                                                                                             derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                46760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                      /note="Sequence from reads from a short insert library
derived from a single pUC clone. Restriction digest
confirm the assembly."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                .46849
                                                                                   0;
                                                                                                            Score 63.6; DB 9;
Pred. No. 8.7e-11;
                                                                                   Mismatches
                                                                                                                                                                                                                         20778 t
                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                       from a clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from a short insert clone. Restriction
                                                                                   29;
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Restriction
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digest o
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VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL137847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 17, 2001 this sequence version replaced gi:16408610.
During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                          sections only once, except for a short overlap. The true left end of clone RP11-439K3 is at 1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chr9
RPI1-439K3 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimberley, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt IMPORTANT}\colon {\tt This} sequence is not the entire insert of clone RP11-439K3 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where differences are found these are annotated as variations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                  Similarity
                                                                                                                                                 42809
                                                                                                                                                                                                                                                                                                                                                                                                   left end of clone RP11-344L17 is
           Conservative
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                                                                                                                                                                                                                                                                                                                                               1. .143372
                                                                                                                                      /clone="RP11-439K3"
/clone_lib="RPCI-11.2"
30224 c 28152 g 42
                                                                                                                                                                                                                             /chromosome="9"
/map="q22.2-31.1"
                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143372 bp DNA linear PRI 16-NOV-2001 sequence from clone RP11-439K3 on chromosome 9q22.2-31.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to 143372)
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                             57.3%;
     0;
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     Score 63.6; DB 9;
Pred. No. 8.7e-11;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UK. E-mail enquiries:
                                                                                                                                              42187
                                                                                                                                                                                                                                                                                                                                                                                             is at 1 in this sequence. at 141373 in this sequence
                                                       Length 143372;
     0;
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Gaps
     0;
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GATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTGGGTCTC 84

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RESULT 8
AL137179/c
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VERSION
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                                                                                                  BASE COUNT
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Best Local Similarity
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                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATAGATTTCCTGCCTTGCCAGGGATCCTGGGGCCCAGAGTATGTAAAACTCCTGGGTCTC 82283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
on Oct 1, 2000 this sequence version replaced gi:9931245.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP11-82M9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-82M9 is at 153053 in this sequence. The true right end of clone RP1-27919 is at 100 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr6
RP11-82M9 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as rollows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
AL137179
AL137179.14 GI:10443372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tracey, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA
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                                                                                                    47748
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                                                                                             /note="Tandem repeat. Forced join. missing according to restriction d 31096 c 30495 g 43714 t
                                                                                                                                                                       /clone_lib="RPCI-11.1"
102234. .102253
                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                         /clone="RP11-82M9"
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                        1. .153053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence from clone
57.3%;
73.6%;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome 6 clone SEQUENCE, 22 unordered niacon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 7, 2000 this sequence version replaced 91:6970573. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                  Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 13528 bases at least Q40 Consensus quality: 141969 bases at least Q30 Consensus quality: 146244 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                     Center project name: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
Insert size: 150000; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                          612_M_16
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RP11~612M16 map 6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2000
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preserved

3603:

14731 14830:

7951 38050:

33484: 28225: 23976: 18601:

43378:

57339: 49741:

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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1152: contig of 1152 bp in length
1153 1252; gap of 100 bp
1253 2252: contig of 1000 bp in length
2253 2352; gap of 100 bp
2353 3503: contig of 1151 bp in length
     /note="assembly_fragment"
6160. .6832
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                 note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ous9: contig of 1301 bp in length 6150: gap of 100 bp 6832: contig of 5000 bp
                                                                                                                              'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                            clone_lib="RPCI-11 Human Male"
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10: contig of 1

10: contig of 1

10: contig of 1

10: contig of 1
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28125: contig of 4149 bp in length
225: gap of 100 bp
33384: contig of 5159 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42: gap of 100 μρ
86960: contig of 12218 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126: gap of 100 bp
74642: contig of 9416 bp in length
42: gap of 100 bp
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49641: contig of 6263 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60: gap of 100 bp
15886: contig of 28826 bp in length
986: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30. gap of 100 bp
18501: contig of 3671 bp in length
01: gap of 100 bp
23876: contig of 5275 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     00: gap of 100 bp
13278: contig of 5228 bp in length
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gap of 100 bp
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contig of 4466 bp in length
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of 1151 bp in length
100 bp
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                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens BAC clone RP11-750022 from 4, AC109592
2 (bases 1 to 86314)
Buatsi,D. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-750022
                                                                                                                            Suiston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                 984707
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                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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/note="assembly_fragment"
a 29588 c 28599 g 45687
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87061. .115886
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49742. .57230
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6933. .9547
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74743. .86960
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115987. .153422
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Submitted (05-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
3 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 9, 2002 this sequence version replaced gi:18642965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-MAR-2002) Genome University School of Medicine,
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4 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 (bases 1 to 86314) Waterston, R.H.
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                                                                                                          The clone sequenced to the left is RP11-510D4, 2000 bp overlap; clone sequenced to the right is RP11-36611, 2000 bp overlap. Actual start of this clone is at base position 149897 of RP11-510D4; actual end is at base position 44359 of RP11-36611.
                                                                                                                                                                                                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. John D McPherson, Department of Genetics, Washington University, St. McPherson and Information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restriction digest.
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----- Summary Statistics
Center project name: H_NH0750022
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/organism="Homo sapiens"
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/chromosome="4"
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1216. .1472
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23095. .23142
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14817. .14883
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256. .655
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29073.
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                                   /rpt_family="AT_rich" 34024. .34352
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29563. .30039
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26979. .27252
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                Birren,B., Linton,L., Nusbaum,C., Lauver,L., Beda,F.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Anderson,S., Boukhgalter,B., Brown,A., Burkett,G., Castle,P.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,P.,
Channel V., Colangelo,M., Collins, S., Collymore,A., Cooke,P.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke, DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertet Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 159475)
Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-26G6
                                                                                                                                                                                                                                                                                                            AC021378 159475 bp DNA Homo sapiens clone RP11-26G6, WORKING I
                                                                                                                 Unpublished
                                                                                                                                                                                                               Homo sapiens.
Homo sapiens
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51158
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42632
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/rpt_family="L1"
39172. .39448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="L1"
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45531. .47107
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43786. .45120
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39523. .39821
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82.0%;
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1. .42895
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Pred. No. le-1
0; Mismatches
                                                                               Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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Gage, D., Galagan, J.,
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               misc_feature
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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On May 25, 2000 this sequence version replaced gi:7637277. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, P., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, P., Pierre, P., Pierre
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150152 bases at least Q40
Consensus quality: 150379 bases at least Q30
Consensus quality: 157415 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 158775; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
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                                                                                                          Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L. Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,
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* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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127026 159475: contig of 32450
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94763 12692
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                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-26G6"
/note="assembly_fragment
                                                                                     /clone_lib="RPCI-11 Human Male BAC"
1. .2315
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126925: contig of 32163 bp in length
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                                             requests: clonerequestésanger.ac.uk
On Nov 8, 2000 this sequence version replaced gi:11071307.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGTGTGTGCCTGAGTGGCTGCTCTACT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGTGTGCCCCCAGTGGCTGCTCTGCT 45677
Group. Further information can be round at http://www.sanger.ac.uk/HGP/Chr9
IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSs and GSSs, complete : AL157937
AL157937.21 GI:11121006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from clone RPI STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimberley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="assembly_fragment"
9142. .17359
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27831 c 28355 g
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127026. .159475
.note="assembly_fragment"
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17460. 26067
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2416. .9041
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94763. .126925
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82.0%;
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The true left end of clone RP11-408N14 is at 1 in this sequence. The true left end of clone RP11-4115 is at 153684 in this sequence. The true right end of clone RP11-145E5 is at 29400 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-408N14 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VECTOR: pBACe3.6.
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7812. .812
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/note="AluJb repeat: matches 1. .304 of consensus"
1671. .2296
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/note="MIR repeat: matches 29.
9360. .9878
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                             /note="LIPAS repeat: matches 76. .6143 of consensus" 17910. .18096
                                                                                                   /note="MIR repeat: matches 139.
11255. .17292
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6538. .6935
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/db_xref="taxon:9606"
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/note="23 copies 2 mer tg 93% conserved"
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   .7835 of
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consensus"
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/note="L1MC4 repeat: matches 7641.

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misc_feature
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                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2627. .2749 of consensus" 48349. .48579
                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS: Em:AQ343245"
47817. .47938
                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 1 .205 of consensus"
complement(46149 .46586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ894025"
40317. .40540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38923. .39151

/note="Charlie4 repeat: matches 231. .1926 of complement(39281. .39766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36624..36669
/note="23 copies 2 mer ta 76% conserved"
36680..36897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1PA13 repeat: matches -248. .1557 36624. .36669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="THE1B repeat: matches 1. .359 of consensus" 33485. .35130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1PA10 repeat: matches 5655. 26120. .26412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="LIPA11 repeat: matches 2262. 25293. .25713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18520, .20148
/note="LIPAI2 repeat: matches -1421, .1009 of consensus"
20127, .21370
/note="LIPAI1 repeat: matches 921, .2161 of consensus"
21372, .25281
                                                                                                                                                                                                                                                       50674.
                                                                                                                                                                                                                                                                                              50262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   45413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluY repeat: matches 1.
45076. .45280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2673. .2750 of consensus" 43962. .44259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 20.
40603: .40726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluY repeat: matches 1..300
complement(27055..27448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26660.
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27407. .31040
                                                                                                                                                                                                                 /note="LIM1 repeat: matches -1389. .30 of consensus"
52084. .52853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2587. .2710 of 43871. .43952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1P repeat: matches 1541.
31144. .31497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSx repeat: matches 3.
                                     /note="L1PA12 repeat: matches 10, .540 of consensus'
                                                                            note="63 copies 2 mer tt 59% conserved"
                                                                                                                  note="MLT1F repeat: matches 346.
                                                                                                                                                                                                                                                                                                          note="MLT11 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 2. .205 of consensus"
45413. .45588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37435. .37508
/note="37 copies 2 mer ag 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MC4 repeat: matches 6404. .6623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="THE1B-INTERNAL repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="THE1B repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1PA12 repeat: matches 2505. .6164 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match: GSS: Em:AQ147782"
                                                                                                                                                                                        note="IlMA2 repeat: matches 5516, .6308 of consensus"
                                                                                                                                                                                                                                                                                              .50664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .31138
                                                                                                                                                                                                                                                                       repeat: matches 2339. .2749 of consensus"
repeat:
                                                                                                                                                     repeat: matches 1. .6146 of consensus"
  matches
7 .
    . 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .234 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .299 of consensus"
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                                                                                                                                                                                                                                                                                                             .220 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1650 of consensus
                                                                                                                  .541 of
  of
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RA MUZNY D.M., Adams C., Bailey M., Barbaria J., Blankenburg K., Bodota B.,
RA Bouck J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J.,
RA Carter M., Chacko J., Chen Z., Cox C., David R., Delgado O., Deshazo D.,
RA Carter M., Chacko J., Chen Z., Cox C., David R., Delgado O., Deshazo D.,
RA Gartel M., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,
RA Ferraguto D., Forcum Tansey J., Frantz P., Ganesh R., Gorrell J.H.,
RA Gorrell L.L., Guevara W., Harris K., Hernandez J., Hodgson A., Hogues M.,
RA Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,
RA Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,
RA Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.,
RA Holloway C., Hosak H., Jackson L., Jackson L., Jia Y., Jones M.,
RA Martinez C., McLeod M.P., Mei G., Morgan M., Morris S., Nash S., Nelson A.,
RA Martinez C., McLeod M.P., Mei G., Morgan M., Morris S., Nash S., Payton B.,
RA Mayyen R., Nguyen S., Oswal G., Parish B., Paxton S., Payton B.,
RA Perez L., Pu Ll., Quiles M., Reiter D., Rives M., Samuel S., Say J.,
RA Scherer S., Shah E., Shen H., Simon M., Sparks A., Stamps A., Sucgang R.,
RA Tabor P., Taylor T., Vasquez L., Vinson R., Vo Q., Wahbah M.,
RA Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,
RA Waren J., Wrensford G., Yu W., Zhou X., Nelson D., Gibbs R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18927 GAGTATGTAAAGCTCCTGGGGTCTCTGTGCATACCTGAGCAGCTGCTCTGCT 18877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
1-123779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Eukaryota; Metazoa;
Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 62, Created)
(Rel. 64, Last updated, Version 11)
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/note="L1PA10: 67317...69162
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64816. .64938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1PA10 repeat: matches 3793. 69122. .69167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1P4 repeat: matches 5616. .5662 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%;
73.0%;
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Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 1. .608 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 1761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matches 539. .-291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5643 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1897 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3818 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0,990329
Consensus quality: 11233 bases at least Q40
Consensus quality: 117272 bases at least Q30
Consensus quality: 119789 bases at least O30
Estimated insert size: 121963; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-JAN-2000) to the EMBL/GenBank/DDBJ databases. Human Genome Sequencing Center, Department of Molecular and Human Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: HMXB
Center clone name: RP11-79K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Aug 7, 2000 this sequence version replaced gi:8700003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Direct Submission";
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley K.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13;
                                                                                                            source
                                   Sequence 123779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE:
                                                                                                                                                                                                                                                                                                                                                                                      as soon as i
                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                 105595
105695
                                                                                                                                                                                                                                                                                                                                           35932
36032
60755
                                                                                                                                                                                                                                                                                                                    60855
71668
                                                                                                                                                                                               .20199
                                                                                                                                                                                                                       12908
                                                                                                                                                                                                                                                                                                                                                                                                       it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                            60854:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    College of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
                                  BP; 37802 A; 24017 C; 23437 G; 37612 T; 911 other;
                                                          /chromosome="3"
/db_xref="taxon:9606"
/organism="Homo sapiens"
/clone="RP11-79K17"
                                                                                                                                   Location/Qualifiers
                                                                                                             .123779
                                                                                                                                                                                                                                                                                                      gap of contig gap of contig
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                                                                                                                                                                                                                                                                                g of 13059 bp in f unknown length of 11795 bp in
                                                                                                                                                                                                                                                         of 8773
                                                                                                                                                                                                                                                                                                                                                        unknown length of 24723 bp in
                                                                                                                                                            of.
                                                                                                                                                                                                                                                                                                                                 of 10813 bp in
                                                                                                                                                                                  of 1922
                                                                                                                                                                                                            of 7191
                                                                                                                                                                                                                                    of 7213
                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                                                                                                                              unknown length
                                                                                                                                                                                                                                                                                                                                                                                of 35931 bp in
  Score 62.4; DB 30;
Pred. No. 2.2e-10;
                                                                                                                                                            1459
                                                                                                                                                          bp in length bp in length bp in length
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bp in
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RESULT 14
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
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                                                   COMMENT
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                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma, J., Mahesiwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Mei, G., Metzker, M., Meal, D., Newtson, J., Newtson, N., Morgan, M., Myuyen, N., Nickerson, E., Neokenkwo, S., Myuyen, A., Nguyen, N., Nickerson, E., Neokenkwo, S., Nguyen, A., Nickerson, E., Neokenkwo, S., Nguyen, A., Nickerson, E., Neokenkwo, S., Nguyen, M., Nickerson, E., Neckenkwo, S., Nguyen, M., Nickerson, E., Nguyen, M., Nickerson, E., Nguyen, M., Nickerson, E., Nickerson, M., Nickerson, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davy-Carroll, L., Dederich, D.A., Delaney, K. R., Delgado, O.,
Davy-Carroll, L., Dederich, D.A., Delaney, K. R., Delgado, O.,
Denn, A.L., Ding, Y. Dinh, H. H., Douthwaite, K. J., Draper, H.,
Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C. C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabsi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hale, S.,
Hamilton, K., Harris, C., Hartis, K., Hart, M., Havlak, P., Hale, S.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hugues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hune, J.,
Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseyed, H., Lozado, R. J., Lu, X., Lucler, R., Luna, R.,
Martin, D., Marchin, M., Marche, D., Martin, D., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTGTGTGCCTGAGTGGCTGCTCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 3 clone 14 unordered pieces. AC076949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
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Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burcch, P., Burkett, C., Burrell, K. L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., David,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Pr
1 (bases 1 to 128118)
Muzny,D.M., Adams,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                   submitted (01-AUG-2000) Human Genome Sequencing Center, Del
of Molecular and Human Genetics, Baylor College of Medicin
Baylor Plaza, Houston, TX 77030, USA
on Oct 14, 2001 this sequence version replaced g1:10047573
                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alsbrooks, S.L., Amaratunge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                  (bases_1 to 128118)
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HASE1; HTGS_DRAFT
Genome Center
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                                                                                                                                                                                  Genome Sequencing Center, Depa
cs, Baylor College of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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DRAFT SEQUENCE,
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 14 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                  72; Conser
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 111307 bases at least Q40
Consensus quality: 117905 bases at least Q30
Consensus quality: 121494 bases at least Q30
Estimated insert size: 122854; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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Center project name: HBRJ
Center Clone name: RP11-79K12
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114250
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4: gap of unknown length
1: contig of 12617 bp in length
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8: contig of 13312 bp in length
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contig of 8927 bp in
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Pred. No. 2
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δð В 20

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30), an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were

ORIGIN

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TITLE
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REFERENCE
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AUTHORS
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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Submitted (16-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 128583)
                                                                                                                                                                                                                                                                              Overlapping Sequences: 5': RP11-147N17 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUN-2002) Genome Center, University of Washington Box 352145, Seattle, WA 98195, USA On May 16, 2002 this sequence version replaced gi:9719675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 12883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphinmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
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Saenphimmachak,C., Phelps,K.A., Buckley,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 128548 bases at least Q40 Consensus quality: 128580 bases at least Q30 Consensus quality: 128581 bases at least Q20 Insert size: 128583; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project Information
Center project name: chr-3
Center clone name: RP11-79K17 (bc0196)
                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 13.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 45% of reads Sequencing vector: M13; L08821; 55% of r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: University of Washington Genome Center
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    Summary Statistics

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Kibukawa, M., Raymond, C.
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covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

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Best Lock Matches Qy 24 1 Db 27328 1 Qy 84 1 Db 27268 Search com Job time :	FEATURES SOURCE BASE COUNT ORIGIN									
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Pred. No. 2.2e-10; 0; Mismatches 16; GACTTCTGGGGCCGAGTAT	L. 128583 L. 128583 L. 128583 Corganism="Homo sapiens" Adb_xref="taxon:9606" Adb_xref="taxon:9606" Aclone="RP11-79K17" Aclone="RP11-79K17" Aclone=ib="RPCI human BAC 24752 c 24789 g 41265 56 23. Score 62 4.				7555	; 1	7644	1098 798	5289	461
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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  AAC03794
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                                                                                                                                      Description
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Probe
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162 22 A S S S S S S S S S S S S S S S S S
ABA75762 ABA63320 AAS68019 AAS68029 AAS69200 AAS829303 AAS827610 AAS77610 AAS77643 AAS77644 AAS77644 AAK74465 AAL11101 AAF1444 AAK74465 AAL16101 AAF1444 AAK74465 AAH1423 AAF1465 AAH1423 AAF16431 AAH4123 AAF16431 AAH4123 AA
DNA encoding novel Human foetal liver DNA encoding novel Human immune yste DNA encoding novel Human breast cance Human breast cance Pyrococcus abyssi Pyrococcus ab

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ALIGNMENTS

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RESULT 1
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ID AAC0
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ACC AAC0
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XX
                                                              WPI; 2000-500381/45.
P-PSDB; AAG03788.
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gene therapy; (
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                                                                                                                                                                                                           26-FEB-1999;
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                                                                                                                                                                                                                                                                                               06-SEP-2000
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                                                                                                                                                                  (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                           Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein 5' EST, SEQ ID NO: 3792.
                                                                                                                                                                                                             99US-0122487
                                                                                                                           'n
                                                                                                                         Duclert A,
                                                                                                                           Giordano
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Probe

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

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RESULT 2
AAZ42680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are
Claim 1; Page 402; 837pp; English
                                        Novel secreted protein diagnostic, forensic, g
                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                 09-APR-1998;
28-APR-1998;
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                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
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forensic; loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST isolated from a cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location; development; ; identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; diagnosis;
chromosome mapping; upstream regulatory sequence;
                                                                                                                                                                                                                                                                 98US-0057719
98US-0069047
                                                                                                                                                                                                                                                                                                                                   99WO-IB00712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71pp + CD-ROM; English.
                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy and chromosome mapping procedures
                                                               5' expressed
                                                                                                                                                                            Duclert
                                        therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111; DB 21;
Pred. No. 1.4e-27;
                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein synthesis; stability;
                                           and chromosom
                                                                                                                                                                            Giordano
                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                  sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO:439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                           mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                           procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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В Ş рb Q

PD PD XXX PF PX XXX PF PX XXX PF XXX

AAZ42265

g

represent novel

5,

expressed sequence tag (EST

Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon

comprises 3351 human

polynucleotidé

sequences

Or a

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RESULT 3
AAF65888/c
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sin
Matches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resulting from abnormal gene expression. The products may also be used i gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences, corresponding to human secreted proteins. AAY64651 to AAY65438 represent the EST-related proteins corresponding to AAZ42265 AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs ca also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases.
                                                                                                       Kita
                                                                                                               Williams LT, Escobedo J, Reinhard C, Randazzo F, Crkenjakov R, Drmanac S,
                                                                        WPI;
                                                                                                                                                                                                                                            02-JUL-1999;
                                                                                                                                                                                                                                                                            30-JUN-2000; 2000WO-US18374
                                                                                                                                                                                                                                                                                                           11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                          WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF65888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF65888 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 447 BP; 74 A; 105 C; 125 G; 138 T; 5 other;
                                                                                                                                                                                   (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGTATGTAAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT
                                                                        2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                     Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Lung
                                                                                                                                                                                                                                99US-0142311
                                                                                                                                                                                                                                             9905-0142310
                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; colon cancer; p
g cancer; cancer detection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                       Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                    Kennedy GC, Pot D,
Dickson M, Labat I
S LW, Strache-Crain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO: 1644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111; DB 21; Pred. No. 1.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                    PD, Klinger J, K, Lamson G, Drman I, Leshkowitiz D;
                                                                                                     В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesis, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                    Kassam
nanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can
                                                                                                                                                   P
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be
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Claim

9;

Page

779;

1046pp;

English

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Sequence
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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, and proposed and proventive disorders such as neoplasia.
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RESULT 4 ABA63453/c Вb Qy DЬ Qy Matches ery Match 01-FEB-2002 ABA63453 standard; DNA; 570 Human foetal liver single exon nucleic acid probe #11758. 74 61 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCCTGCTCTACT 111 1 ATGGGTGGATCTTTTGCAGGACTTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCG 60 ocal GAGTACGTAAAGCACCTGGGTCTCTGTGCATGCCTGAACAGCTGCTCCCCT 78; Similarity 349 BP; 90 A; 93 C; Conservative (first entry) 52.4%; 70.3%; 0; Score 58.2; Pred. No. 7. 102 G; 64 T; 0 other; Mismatches .1e-10; ω ω •• Length Indels 24 0; Gaps

0;

δÃ Дb Qy

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EXX SX DX DX AC
09-AUG-2001.
                     Homo sapiens
                                 foetal
                                 gene expression; single exon nucleic
                                 acid
```

probe;

SS

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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                              WPI; 2001-483447/52.
                                                                                     04-OCT-2000;
                                                                                                                                         30-JAN-2001; 2001WO-US00669
                                                                                                  21-SEP-2000;
                                                          SG,
                                                                        MOLECULAR DYNAMICS INC
                                                          Hanzel
                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                          DK,
                                                          Chen W,
                                                           Rank
                                                          DR,
```

analyzing

SEQ gene

ID NO 11758;

relates to a single exon nucleic acid probe for

639pp + sequence listing; English.

genome-derived single

expression

ij

exon nucleic n human fetal

acid liver

probes useful

measuring human gene expression in a sample derived from human heart. The prosent sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

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RESULT 5
ABA30652/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetal liver. The present sequence is a single connected of the invention.

Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 570 BP; 169 A; 154 C; 156 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene expression; heart; microan cardiovascular disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #9118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA30652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA30652 standard; DNA; 570
                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566
                                         Claim 1;
                                                                                                       Single
The present invention relates to single exon nucleic acid probes
                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 Treference Greekerge Colored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 GGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCCTGGGTCT
                                                                                                                                                                                             SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGTGTGTGCCTGAGTGGCTGCTCTAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATGGATCTCCTGCCTTGCTGGGATTCCTTGGGCTGGAGTATGTAAAATTCCTGGGTCT 507
                                                                                                                                                   2001-488899/53
                                                                                                       exon nucleic acid probes
                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                       SEQ ID No 9118; 530pp; English
                                                                                                                                                                                             Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                            ; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
                                                                                                                                                                                                                                                                                ; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                          DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.48;
79.38;
                                                                                                                                                                                             Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart; microarray; vascular system; hypertension; cardiac arrhythmia;
                                                                                                                                                                                             Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58.2; DB 22; Pred. No. 8.2e-10; No. 8.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . вр
                                                                                                                                                                                             Rank
                                                                                                       for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                             DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 6
11985/c
                                                                                                                                                                                                                                                21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; Alzheimer's disease; multiple
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 570 BP;
                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                           WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK11985
                                                                                                                                                                Single exon nucleic acid probes
                                                                                                                                                                                      WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                  03-AUG-2000;
                              Sequence 570
                                                                                                                                    Example 4; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566
                                                                                                                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTGTGTGCCTGAGTGGCCGCTCTGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTGTGTGCCTGAGTGGCTGCTCTAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                           Hanzel
                                                                                                                                                                                                                                                           ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                               BP;
                                                                                                                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 A; 154 C; 156 G;
                                                                                                                                                                                                           DK,
                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.4%;
                              A; 154 C;
  52
79
                                                                                                                                    11976; 650pp + Sequence Listing;
                                                                                                                                                                                                           Chen
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Pred. No. 8.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
 Score
Pred.
                              156 G; 91
                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                  for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe
  NO
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 T; 0
  . 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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 DB 22;
.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
          Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11976
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                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                         probe;
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B

506

480

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AAK37688/c
ID AAK37688 standard; D
XX
AC AAK37688;
XZ AAK37688;
XX DT 06-NOV-2001 (first
XX DT 06-NOV-2001 (first
XX Human bone marrow ex
XX KW Human; bone marrow ex
XX Human; bone marrow ex
XX WO200157276-A2.
XX 09-AUG-2001; 2000US-
PR 30-JAN-2001; 2000US-
PR 26-MAY-2000; 2000US-
PR 26-MAY-2000; 2000US-
PR 27-SEP-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 04-OCT-2000; 2000US-
PR 04-OCT-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 10-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 11-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 31-SEP-2000; 2000US-
PR 31-SEP-2000; 2000US-
PR 31-SEP-2000; 2000US-
PR 31-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 31-SEP-2000; 2000US-
PR 31-SEP-20
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                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone {\tt marrow} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed single exon probe
                                                                                                                                                                                                                                                                                  Sequence 570 BP; 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506
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                                                                                      TIGIGIGICCIGAGIGCCCCTCIGC
                                                                                                                                       GGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGGCCGGAGTATGTAAAACTCCTGGGTCT
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                                                 CTGTGTGTGCCTGAGTGGCTGCTCTAC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; Leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                      Conservative
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2000US-0236359
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2000US-0632366
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2000US-0207456
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                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                               52.4%;
                                                                                                                                                                                                                                                                                    A; 154 C; 156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12245; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
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                                                                                                                                                                                           0;
                                                                                                                                                                                      Score 58.2; DB 22; pred. No. 8.2e-10; 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphoma; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                        Length
                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                             570;
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507
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                                                                                                     507
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RESULT 9
AAI43563/c
ID AAI43563;
XX
AC AAI43563;
XX
DT 17-OCT-20;
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AAI18447/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; human; microarray;
    17-OCT-2001
                                            AAI43563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #8380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI18447;
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                                                                                                                                                                                                                                                                           GAATGGATCTCCTGCCTTGCTGGATTCCTTGGGCTGGAGTATGTAAAATTCCTGGGTCT 507
                                                                                                                                                                                                                                                                                                 GGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTGGGTCT
                                                                                                                                                                                              TTGTGTGCCTGAGTGGCCGCTCTGC
                                                                                                                                                                                                                  CTGTGTGTGCCTGAGTGGCTGCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid probes useful zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                             l Similarity 79...
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 570
                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 8380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to human single exon nucleic acid probe present sequence is one such probe. The SENPs are derived HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
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                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                   52.4%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 154 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression analysis in human cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                        570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570
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                                                                                        ВP
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                                                                                                                                                                                                                                                                                                                                                             Score 58.2; DB 22;
Pred. No. 8.2e-10;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                               156 G; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression;
                                                                                                                                                                                              480
                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                       570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell
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                                                                                                                                                                                                                                                                                                                                                               0;
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derived
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                               0,
RESULT 10
ABS11680/G
ID ABS11
XX ABS11
XX ABS11
XX 19-AU
DT 19-AU
XX Human
XX Human
KW Chron
KW famil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 506
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Query Match
Best Local S
Matches 69
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
Hermansky-Pudlak syndrome; sarcoidosis; pulmonary histocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #12249 used
                                                                   Human; ds; single exon probe; asthma; lung cancer; COPD; ILD chronic obstructive pulmonary disease; interstitial lung dis familial iddiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 570 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                       ABS11680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                       84 CTGTGTGTGCCTGAGTGGCTGCTCTAC
                                                                                                                                                                                                                                                                                                                                                                GGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTGGGTCT
                                                                                                                                                                                                                                                                                           TTGTGTGCCTGAGTGGCCGCTCTGC
                                                                                                                                                                                                                                                                                                                                                GAATGGATCTCCTGCCTTGCTGGGATTCCTTGGGCTGGAGTATGTAAAATTCCTGGGTCT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-488897/53
                                                                                                                                     genome-derived single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234687.
; 2000US-0234683.
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 A; 154 C; 156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No 12249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to measure gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                         570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654pp; English.
                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                    Score 58.2; DB 22
Pred. No. 8.2e-10;
); Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                                                                     110
                                                                                                                                       probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 T; 0 other;
                                                                                                                                     from lung
                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis;
                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                       H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isplaying gene
probes are useful
                                                                                                                                        No 11671
                                                                                                                                                                                                                                                                                                                                                                                                                                 570;
                                                                                                disease
                                                                                                           ILD;
                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sample.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SENP)
                                                                                                                                                                                                                                                                                                                                                                            83
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Homo sapiens.

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the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Nemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histocytosis, lunghangioleiomyomtosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several these contents are all the expression of each of the exons in several
                                           of the printed specification, but was format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid probes for measuring gene expression in a sample derived
from human lung comprising single exon nucleic acid probes having one
12614 nucleic acid sequences mentioned in the specification, or their
complements or the 12387 open reading frames derived from the 12614
                                                                                                                              Note: The sequence data for this
                                                                                                                                                                          probe of the invention
                                                                                                                                                                                                                                                                                           pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
    ttp.wipo
                                                                                                                                                                                                                                                    pulmonary dysplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                                                                                             nonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension hyaline membrane disease. The present sequence is a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 11671; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-234687P.
2000US-236359P.
2000GB-0024263.
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2000US-207456P.
2000US-0608408.
2000US-0632366.
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                                                                                                                          patent did not form part
                                                                                                                                                                                                        present sequence is a single
                                                                                  obtained
                                                                                  uŢ
                                                                              electronic
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of.

Query Match Best Local Similarity

52.48; 79.38; A,

Score 58.2; DB 24; Pred. No. 8.2e-10;

Length 570;

Sequence 570

BP;

169

154 Ç;

156

G; 91

T; 0 other;

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ABK83461/c
ID ABK834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
(GCA), by detecting the level of expression of gene(s) (GS) identified by CC DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated CC GC, where differential expression of GS is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in GS; (2) screening (M3) CC for an agent tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammation or inflammation; (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammation or inflammation; (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, and the subject is inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA; M2 is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungal infection; sterile inflammatory disease; psoriarheumatoid arthritis; glomerulonephritis; asthma; throcardiac reperfusion injury; renal reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral infection; parasitic infection; protozoal fungal infection; sterile inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beazer-Barclay Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK83461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK83461 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTGGGTCT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGGATCTCCTGCCTTGCTGGGATTCCTTGGGCTGGAGTATGTAAAATTCCTGGGTCT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte activation by detecting differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-237189P
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                                                                                                                                                                                                                                                                                                                                                                                                                      relates to detecting (M1) granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA; 128600
                                                                                                                                                                                                                                                                                                                                                                                                                                                            114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM, Yamaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vockley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                      (GC)
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RESULT 12
AAC68089/c
ID AAC68089 standard; cDNA; 1982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 126322 ATGTGTGGACCTCCCACCTTGACTTCATTGCAGACGCATTTGTTGGGGGCTCCTGGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renactive reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, confiammatory bowel disease, Crohn's disease, ulcerative colitis, confiammatory bowel disease, crohn's disease, ulcerative colitis, confiammatory bowel disease, crohn's disease, ulcerative colitis, confidential disease; also bacterial infection, viral infection and M5 is confidential protocoal infection, fungal infection and M5 is constituted in the crompton one of the above conditions. The present consequence for the above conditions. The present consequence data for this patent did not form part confidentially expressed in granulocytes. Consequence data for this patent did not form part confidentially expressed in granulocytes. Consequence data for this patent did not form part confidentially expressed in granulocytes. Consequence data for this patent did not form part confidentially expressed in granulocytes. Consequence data for this patent did not form part confidentially expressed in granulocytes. Consequence data for this patent did not form part confidentially expressed in granulocytes.
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                                                      Nucleic acids encoding ameliorate or diagnose diseases e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antidicer; vulnerary; antionvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
              Claim 1; Pages 321-322;
                                                                                                                                                                           WPI; 2000-611702/58
                                                                                                                                                                                                                        Rosen CA,
                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCT 106
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75; Conser
                                                                                                                                                        AAB37356
                                                                                                                                                                                                                   Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US07534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                99US-0126598.
99US-0171504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein cDNA sequence #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36139 A; 24970 C; 26316 G; 41175 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.8%;
                                                                                                                                                                                                                   Komatsoulis
                                                                                human secreted conditions suc
         387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombosis, cardiac reperfusion injury, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                such
                                                                                                 proteins, used to treat, prevent
                                                                              as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                            cancer, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The invention relates to the isolation of genes AAC68081-C68127 encoding CC 47 human secreted proteins AAB37348-B37394. The genes can be used to CC generate fusion proteins by linking to the gene for the human CC generate fusion proteins by linking to the gene for the human CC immunoglobulin G FC portion (AAC68072) for increasing the stability of CC the fusion protein as compared to the human protein only. The genes and CC proteins are useful for preventing, ameliorating or treating medical CC conditions, e.g. by protein or gene therapy. The genes are isolated CC rucleic acids, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and ceptilepsy; and (f) infectious diseases such as viral, bacterial, fungal and infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                                                            25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                           P-PSDB;
                                                                                                      Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1103
                                                                                                                                (HYSE-)
                                                                                                                                                                                                                                                                02-AUG-2001
                                                                                                                                                                                                                                                                                              WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1163
                                                                                                                                                                                                                                 25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                                                                                                                                  diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                      biodiversity;
                                                                                                                                                                                                                                                                                                                                                                                                 Human; sheep; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human EST-derived coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH98980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH98980 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy; and and parasitic
                                                                                                                                                                                                                                                                                                                                                                                   tomato; monkey;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                           2001-476164/51
DB; AAM24321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCTGCTGGGTCTCTGCACGTGCTCAAGCGGCTACTCTGCT 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTCTACT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTCCCGCTTTGCAGGAGTTGCAGTTACTTTTGCTGGGAAACCCAGGGCCGGAGTATGT 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCTTTTGCCTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGGCCGGAGTATGT
                                                                                     , Liu C,
Drmanac |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Similarity
73; Conser
                                                                                                                                HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections.
                                                                                      RA,
                                                                                                                                                                                                                                                                                                                                                                                   dog;
                                                                                                 Zhou
                                                                                                                                                                                                                                                                                                                                                                                                 cow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA;
                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                                                                   sea urchin;
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70.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                 fruit fly; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609
                                                                                   Qian
J, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55;
                                                                                     Werhman
                                                                                                    XB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                  Wang
nan T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                            hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                                                                             837.
                                                                                                 Chen
       diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1982;
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Claim 1;

Page 694; 1275pp; English

The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess blodiversity and for nutritional purposes. The present sequence is a cDNA of the taggetter.

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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                              New isolated polynucleotide and encoded polypeptides, us
diagnostics, forensics, gene mapping, identification of
responsible for genetic disorders or other traits and to
biodiversity
                                                                                                                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic 
                                                                                           The invention
                                                                                                                   Claim
                                                                                                                                             biodiversity
                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ
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                                                                                                                                                                                                                         2001-639362/73.
                                                                                                                   1;
                                                                                                                                                                                                              ABG27640.
                                                                                                                                                                                                                                                     RT,
                                                                                                                     SEQ
                                                                                                                     IJ
                                                                                                                                                                                                                                                   Liu
                                                                                                                                                                                                                                                                                                      2000US-0649167
                                                                                                                                                                                                                                                                                                                  2000US-0540217.
                                                                                                                                                                                                                                                                                                                                            2001WO-US08631
                                                                                                                                                                                                                                                                             INC.
                                                                                        relates to isolated polynucleotide (I) and
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                                                                                                                     27631;
                                                                                                                  103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic disorder; ss
                                                                                                                                                                                   useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensic;
                                                                                                                                                           mutations
o assess
                                                                                                                                                                                     in
                            techniques
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique

techniques

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RESULT 15
AAS64647/c
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CCCCCXxxxiii
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Best Local
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS64647 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1299
                                                                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS64647;
                                                                                   Claim
                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                Drmanac
                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2
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                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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AAS91827, ID AAS9

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(first

entry)

DNA encoding novel human diagnostic protein #27631.

RESULT 14

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CCTGGGTCTCTGTGTGTGCCTGAGTGGCTGCTGCTAC

CCTGGGTCTCTGTATGTGCCTGAGCACCGGTTCTTC 367

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Query Match Best Local Matches

69;

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Similarity

47.6%; 71.9%;

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609

BP; 99 A; 162

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175

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other;

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to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the inventod not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 807 BP; 224 A; 213 C; 190 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                           9 ATCTTTTGCCTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCCGGAGTATGT 68
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Search completed: April 25, 2003, 01:55:16 Job time: 166 secs 밁 δÃ 망 Ouery Match 41.4%; Score 46; DB 23; Length 807; Sest Local Similarity 65.7%; Pred. No. 1.1e-05; tches 67; Conservative 0; Mismatches 35; Indels

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ALIGNMENTS

	JOURNAL MEDLINE COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AQ770688 LOCUS DEFINITION
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong	Scanning the numan genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 9380589 Contact: Mahairas GG, Wallace JC, Hood L	Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L. Sequence-tagged connectors: A sequence approach to mapping and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 470) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	AQ770688.1 GI:5648804 GSS. human. Homo sapiens	AQ770688 AQ770688 AQ770688 BS_CO8_SP6E RPCI-11 Human Male BAC Library Homo sapiens

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RESULT 2
AQ165256
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3025 row: N column: 12
                                                                                                                                                                                                                     401 Queen Anne Avenue North, Tel: (206) 616-3618 Fax: (206) 616-3887
                                                                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                              scanning the human genome Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ165256 525 bp DNA HS_3025_B2_G06_T7 CIT Approved Human Gen sapiens genomic clone Plate=3025 Col=12 AQ165256
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 944 row: F column: 16
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Location/Qualifiers
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a 112 c 131 g 141 t 3 others
/clone="Plate=3025 Col=12 Row=N"
/clone_lib="CIT Approved Human Genomic
                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="Plate=944 Col=16 Row=F"
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-12 Row=N, DNA sequence.
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TCTGTGTGCCCCCAGTGGCTGCTCTGCT 310
                          TCTGTGTGTGCCTGAGTGGCTGCTCTACT 111
                                                          AGGATGGATCTTCTGCCTTGGCGGGAATCCTGGGGCTGGAGTATGTAAAACTCTTGGGTC 339
                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattl Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3109 row: B column: 11 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103;
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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E-Coli DH10B"
a 155 c 122 g 93 t 5 others
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E-Coli DH10B"
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3109 Col=11 Row=B"
                                                                                                                                                                                                                                    /sex="male"
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RESULT 5
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HS_3077_A1_G04_MR CIT Approved Human
Colmplete=3077 Col=
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Class: BAC ends
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401 Queen Anne Avenue North, Seattle,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                             EST
                                                                                                                         mRNA sequence.
BG675164
BG675164.1 GI:13906560
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Location/Qualifiers
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AQ182486.1 GI:3579853
                                                                            Homo sapiens
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                                 (bases 1 to 867)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 616-3618
(206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="Plate=3077 Col=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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uman Genomic Sperm Library D Homo
Col=7 Row=M, DNA sequence.
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IMAGE:4755296 5',
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                                                           Euteleostomi;
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Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceëu.washington.edu
Elones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact pletter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (lifo@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ457001 516 bp DNA linear GSS
HS_5151_A1_G09_T7A RPCI-11 Human Male BAC Library Homo
genomic clone Plate=727 Col=17 Row=M, DNA sequence.
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Plate: LLAM10617 row: o column: 09
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 516)
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                                                                                                                                                                                                                                  High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                            99380589
                                                                                                                                                                                                                                                                                                                                                                                                             Hood, L.
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/db_xref="taxon:9606"
/clone="mAGE:4755296"
/clone="lib="NGCI_CGAP_SKN3"
/lab_host="DH10B (T1 phage-resistant)"
/note="organ: skin; Vector: pcMv-SpORT6; Site_1: NotI;
/note="organ: skin; Vector: pcMv-SpORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 1.5kb, Library constructed by Lif
Technologies. Note: this is a NCI_CGAP Library."
35 a 208 c 217 g 157 t
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1. .867
.htsc.washington.edu
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73.0%;
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Pred. No. 9.2e-09;
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RESULT 7
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Seq primer: T7
Class: BAC ends
Class: BAC ends
High quality sequence stop: 51f
High quality sequence stop: 51f
High quality sequence stop: 51f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80;
                                                                                                                                               Email: jwallace@l.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ881246 11 DNA linear HS_5137_B1_F08_T7 RPCI-11 Human Male BAC Library Hom genomic_clone Plate=8905 Col=15 Row=L, DNA sequence.
                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seati Tel: (206) 616-3618

Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                               Plate: 8905 r
Seq primer: T7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                    High quality sequence stop: 529
Location/Qualifiers
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                                                                                               BAC ends
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a 126 c 145 g 151 t 8 others
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/db_xref="taxon:9606"
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/Clone_lib="RPCI-11 Human Male BAC Library"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                   row: L
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72.1%;
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                                                                                                                                 column: 15
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Male BAC Library Homo sapiens
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nes 31;
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                                                                                                                                                                                                                                                                                                                                                                                         Hood
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g,J., Zhao,S.,
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RPCI-11-316J23.TV RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other_GSSs: RPCI-il-316J33.TJ
Contact: Shaying Zhao, William Nies
Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ506984.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 597)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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/clone_lib="RPCI-11 Human Male BAC Library"
                                                   /note="vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
161 c 159 g 119 t
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:7621198"
/db_xref="taxon:9606"
/clone="RPCI-11-316J23"
                                                                                   /cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                         /sex="Male"
                                                                                                                                          /clone_lib="RPCI-11"
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Primates;
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Pred. No. 1.6e-07
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Length 597;
                                                                                          Site_2: EcoRI;
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Best Local
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                                                                                                                       1 ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGGCCG
                                               GAGTATGTAAAACTCCTGGGTCTCTGTGTGTGTGCCTGAGTGGCTGCTCTACT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTATGGACCTTCGACCTTGCCTGAGTTGCAGTCATCTTTGTCAGGGATCCTGGGCTCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGATGGATACTTCTCCCACCTTGATGGAGATCCTGGAGCCAGAGTGTGTAAAACTCCTA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 416)

Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Vente.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Other_GSSs: RPCI11-12L15.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of BAC End Sequences for
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71; Conservative
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301 838 0208
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                                                                                                                                                                                                                        /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
103 c 120 g 117 t
                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="RPCI-11-12L15"
/clone_lib="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:7504502"
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                                                                                                                                                                52.4%;
70.3%;
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                                                                                                                                                   Score 58.2; DB 17;
Pred. No. 2.3e-07;
0; Mismatches 33;
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0; Mismatches 21;
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                                                                                                                                                 0;
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AQ193128/c
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Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                      CTTGAGTGACTGCTCTGCT 341
                                                     Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 448)
                                                                                                                                  AQ702903
AQ702903.1
GSS.
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AQ193128.1
GSS.
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                             Mahairas, G.G., Wallace
Keller, A., Shaker, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A0193128 530 bp DI
HS_3060_B1_E08_MF CIT Approved Human
sapiens genomic clone Plate=3060 Col-
   Sequence-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome Proc. Natl. Acad. Sci. U.S.A.
                   Hood, L
                                                                                                                    numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 3060 ro
Class: BAC ends
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: sperm;
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="Plate=3060 Col=15 Row-J"
/clone_lib="CIT Approved Human Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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83.5%;
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                                             Wallace, J.C.,
                                                                        Chordata;
Primates;
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                              Furlong, J.,
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                                             Smith, K.,
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                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                             Young, J.,
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                          Swartzell,S.,
g,J., Zhao,S.,
approach
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                          Holzman,T.,
Adams,M.D. a
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scanning the human genome

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTGTGTGCCTGAGTGGCTGCTCTGC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1028 row: P column: 3
                                                                                                                                                                                                                                                                                                                                                                                                      AQ899390 769 bp DNA HS_5234_Al_E09_SP6E RPCI-11 Human Male BAC genomic clone Plate=9002 Col=17 Row=I, DNA
                                       High Throughput Sequencing University of Washington
                                                                                                                                        Sequence-tagged connectors: A sequence approach scanning the human genome
                                                                                                                                                                                                     l (bases 1 to /טץ)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
"-יייי chaker.R. Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 769)
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Location/Qualifiers
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                                                                                 Contact: Mahairas GG, Wallace JC,
                                                                                                      99380589
                                                                                                                                                                                      Hood, L
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                        Homo sapiens
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Queen Anne Avenue North, (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
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                                                                                                                       Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
Male blood DNA was isolated from one randomly chosen
and partially digested with a combination of EcoRI an
EcoRI Methylase. Size selected DNA was cloned into th
pBACe3.6 vector at EcoRI sites"
104 c 126 g 140 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1028 Col-3 Row=P"
/clone_lib="RPCI-11 Human Male BAC Library"
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Best Local Similarity
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Clones are derived from the human BAC library RPCI-11. For BAC
library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderiag_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                                                                                         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                           Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
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Seq primer: SP6
                                      Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Other_GSSs: RPCI11-73J15.TV
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Location/Qualifiers
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Seq primer: SP6
Class: BAC ends
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/clone="Plate=9002 Col=17
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76.3%;
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AUTHORS
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                                                                                                                                                                                                                                                                                                 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (lnfo@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Conservative
                                                                                                                                                                        High quality sequence stop: 410 Location/Qualifiers
                                                                                                                                                                                                                                    Plate: 713 row: K column: 23
Seq primer: SP6
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Plate: 713 row: K column: 23
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ442274 410 bp DNA linear GSS HS_137_A1_F12_SP6E RPCI-11 Human Male BAC Library Homo genomic clone Plate=713 Col=23 Row=K, DNA sequence. AQ442274 AQ442274.1 GI:4553613 GSS.
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/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
108 c 118 g 112 t
      Male blood DNA
                                                              /organism="Homo sapiéns"
/db_xref="taxon:9606"
/clone="phate=713 Col=23 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
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/clone="RPCI-11-73J15"
/clone_lib="RPCI-11"
/sex="Male"
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/db_xref="GDB:7527878"
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                                              /sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/ale blood DNA was isolated from one randomly chosen donor
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Pred. No. 3.5e
0; Mismatches
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3.5e-07;
nes 19;
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Best Local Similarity
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99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ437684 453 bp DNA linear GSS 31-MAR-HS_5137_A2_H06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=713 Col=12 Row=0, DNA sequence.
                                                                                                                                                                                                                                                                                                                                          High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                          library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 713 row: O column: 12
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1 (bases 1 to 453)
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For
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a 111 c 111 g 107 t 1 others
                                                                           /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

127 c 117 g 124 t 1 others
                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11 Human Male BAC Library"
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Score 57.2; DB 17; Pred. No. 4.7e-07;
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ch com	174	85	114	25	Matches
Search completed: Ap Job time : 1045 secs	TGTGTC	TGTGTC	GATGG	GATTCI	68;
Search completed: April 25, 2003, 02:28:38 Job time : 1045 secs .	TGTGTGTGCCTGAGTGGCTGCTCCC 199	85 TGTGTGTGCCTGAGTGGCTGCTCTAC 110	114 GATGGTTCTTCTGCCTGCTGCTGATCCCAGGGCCAGAGTATGCAAAATTCCTGGGTCTC 173	25 GATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTGGGTCTC	68; Conservative
3, 02	TCTGC	TCTAC	CTGAT	GGACT	0;
:28:38	199	110	CCCAGGGCCAGA	TCTGGGGCCGGA	0; Mismatches
			STATEC	STATGI	18;
			AAAATTCCT	AAAACTCCT	18; Indels
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4 US-09-078-294-4
US-09-078-294-3
1 US-08-222-177h-4
2 US-08-666-367B-4
4 US-09-143-43B-4
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4 US-08-961-527-34
4 US-08-961-527-34
2 US-08-9428-713-1
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3 US-08-904-179-9
4 US-09-620-412C-136
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2 2 78-294-3	AGGAT	Match .ocal Simi .s 48;	1 178-294-4 2006 4, Application to 6.265211 2015 ANT INFORMATION: JICANT: Choo, Kong JICANT: Choo, Kong JICANT: Du Sart, JICANT: David ZENT FILING DATE: ZENT FILING DATE: ZENT FILING DATE: JENT JENT JENT JENT JENT JENT JENT JENT		222222 232323 24444 44444		ωωω
APTION: APTION	TCTTTTTC.	larit Conse	Applicatio 62652101 Choo, Kong Choo, Kong LD Sart, D Cancilla, REMCE: Davie PLICATION: A REMCE: Davie PLICATION NOS: PATENTIN Ve 1 1008: PATENTIN Ve 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		21.1 21.1 21.1 21.1 21.1 21.1 21.1 21.1		
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/0907 g And ee ael R EL NU 1 1 1 05-1	rgcag ACTG GTG	% of the contract of the contr	en 0 05 Eel 209		84448134	4 4 U U U 4 4	2444
1078294 andy R. R. NUCLEIC ACID MOLECULE US/09/078,294	GGAC GGCC 104	Score 27.6; DB 4; Pred. No. 5.3; 0; Mismatches 34;	/09078294 g Andy ee el EL NUCLEIC ACID MOLECULE F: US/09/078,294 -05-13 .0	ALIGNMENTS	09-059-369- 08-998-416- 08-998-416- 09-123-030- 09-123-0369- 09-059-369- 08-252-9668- 08-290-731C- 09-221-298-	-08-781-891-7 -09-791-211-3 -09-627-376-3	T-US95-13041-1 -08-961-527-51 -08-961-527-29 -09-734-030-3 -08-687-080-10
	TTCTGGGGCCGGAGTATGTAAAACTCCTGGGTC 82 	Length 80246; Indels 0; Gaps (2e 19 2e 19 2e 3, 2e 3,	20 1, 20 51, 20 29, 20 3, 20 3,

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US-08-222-177A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Nucleotide sequence of HC-contig US-09-078-294-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 48; Conserv
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                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENOTH: 175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
APPLICANT: Weber, James L.
                                               FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quence 4, Application US/08222177A
tent No. 5582979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                              POSITION IN GENOME:
                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6678
                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
 OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                              CHROMOSOME/SEGMENT:
                                                                                                                                                            TISSUE TYPE:
                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/341,562 FILING DATE: 21-APR-1989
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                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                         ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Ca
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
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                                                repeat_region 82..128
                                                                                                                                                                                                                                      linear
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                                                                                                                                                          Blood
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/rpt_type= "tandem"
/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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Pred. No. 5.3;
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RESULT 4
US-08-666-367B-4/c
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                                                                                                                                                                                                                                                  Sequence 4, Application US/08666367B Patent No. 5854042
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                     Patent NO. JOURNATION:
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Abundant Class of
                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
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                                                COUNTRY: UZIP: 20005
                                                                                STREET: 805 Fift
CITY: Washington
STATE: D.C.
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                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                               62 AGTATGTAAAACTCCTGGGTCTCTGTGTGTGCCTGAGTGGCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGES: 388-396
DATE: 1989
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Only one strand sequenced"
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTTTGCTGGTGTTTTGTTCAGGATTTTTGTGTATATGTTCATCAAGGATATTGTCCTG 72
                                                                                                                                                                                                                                                                                                                                                 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : May, Paula E.
Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  locus
                                                                                                              E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                 U.S.A.
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May, P. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids
IBM Compatible
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1..175
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58..76
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               Diskette,
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/standard_name= "PCR primer"
/citation= ([1])
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/standard_name= "PCR primer"
/citation= ([1])
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Pred. No. 1
                 inch, 1.44
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CURRENT APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

August 19, 1996

US/08/666,367B

OPERATING SYSTEM: SOFTWARE: Wordper

Wordperfect 5.1

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US-09-143-438-4/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shuich
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/666,367
FILING DATE: August 19, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                   MEDIUM TYPE: Diskette, 3.5
CONPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-371-8850
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    780 GCT 778
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                                                                           APPLICATION NUMBER: FILING DATE: August
                                                              CLASSIFICATION:
                                                                                                                                                                                                                                 STREET: 2033 K S CITY: Washington STATE: D.C.
                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 GGT 81
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                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mouse
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTG 78
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                                                                                                                                                                                                                                                            E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                         Shuichi TSUJI et al.

/ENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR PROTION: PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                       UMBER: US/09/143,438
August 28, 1998
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                                                                                                                                                                    3.5 inch, 1.44 mb
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US-08-961-527-34/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                      TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3
COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
                                                                                                                                                              PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTODAYS ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                              REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: doub
                         LENGTH:
                                                                                   TELEPHONE:
                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410 Ker
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 GGT 81
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                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                              Maryland
                        13104 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                      9410 Key West Avenue
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                                                                                   (301)
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                                                                    309-8512
                                                                                  309-8504
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Pred. No. 3.
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Query Match
Best Local Similarity
Watches 37; Conserv
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US-08-961-527-34
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APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 254
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CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 430
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                  equence 1, Application US/08991840A atent No. 6261570
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LOCATION: (1)...(430)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                     TITLE OF INVENTION: Live Attenuated Virus Vaccines for Eastern Equine Encephaliti:
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: USA MRMC - MRMC-JA
CITY: FORT DETRICK, FREDERICK
                                                                                                                                                                                                                                                                                                                        APPLICANT: Michael D. Parker
APPLICANT: Jonathan F. Smith
APPLICANT: Bruce Crise
APPLICANT: Mark Steve Oberst
                                                                                                                                                                                                                                                                                                          PPLICANT:
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                                                                                                                                                  COUNTRY:
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                                                                                                                                    21702-5012
                                                                                                                                                                       MARYLAND
                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                          Bruce Crise
Mark Steve Oberste
                                                                                                                                                                                                                                                                                                          Shannon Schmura
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                                                       Macintosh 7.5
US/08/991,840A
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Pred. No. 8.6;
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Best Local (
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: Provisio
FILING DATE: May 20, 1997
APPLICATION NUMBER: Provisio
FILING DATE: July 24, 1997
ATTORNEY_AGENT INFORMATION:
NAME: Charles H. Harris
TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7692 TTTGGCTTGGGAGCACTCTTCTTCTTCTTCGGCGGCGGACCTGGCGGCGGATTAGGTGA 7634
                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: N at all occurences is - unknown FEATURE: OTHER INFORMATION: K at all FEATURE: occurences is - G or T
                                                 REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                  FILING DATE: 23-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                COUNTRY: United
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box CITY: Alexandria
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                                                                                                                                     APPLICATION NUMBER: US 08/125,222 FILING DATE: 23-SEP-1993
                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOOK,
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                                   (703)
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                                                                                     30,427
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Pred. No. 16;
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LENGTH:

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; MOLECULE TYPE:
US-08-904-179-1
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Best Local :
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                                                                                                                                                                                                                      TELEFAX: (703) 836-20: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ULT 10
08-904-179-1/c
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SIGNAS, Lars Christer TITLE OF INVENTION: FIBRONECTIN | NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
    322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 CTGAAGGTTCTGACGGTATCAGTG 239
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                                                                                                                                                                      TENGTH: 1371 Dase r
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 25-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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les 47; Conserv
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TCTGACCACCAAGATTATTTTCTCCCTCTGTTGGACCTTCTGGTGTTGATGTCTCTGGAA 263
                           TTTGCCTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGGCCGGAGTATGTAAAA 72
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                                                            l Similarity
47; Conser
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LINDGREN, Per-Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
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                                                         Score 24.8; E
Pred. No. 12;
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                                                                                      Length 1371;
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US-08-428-713-9/c
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                                                                                                                       Matches
                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILLING DATE: 23.5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1374 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                               FEATURE:
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 262
                                                          322 TCTGACCACGAAGATTATTTTCTCCCTCTGTTGGACCTTCTGGTGTTGATGTCTCTGGAA 263
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rea, Teresa Stanek REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/428,713 FILING DATE: 25-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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CTGAAGGTTCTGACGGTATCAGTG 239
                                                                                       TTTGCCTTGCAGGATTCTTTTCATCTTTGCAGGGACTTCTGGGGGCCGGAGTATGTAAAA 72
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                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 1404
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LINDGREN, Per-Eric
                                                                                                                                                                                                                                                                                                                                                      (703)
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                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burns,
                                                                                                                                                                                                                                                                                                                                                                   (703) 836-6620
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                                                                                                                                  Score 24.8;
Pred. No. 12;
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                                                                                                                       Mismatches
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                                                                                                                                                  Length 1374;
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RESULT 12 US-08-904-179-9/c

0;

Sequence 9, Application US/08904179 Patent No. 6086895

GENERAL INFORMATION:

APPLICANT:
APPLICANT:

APPLICANT: SIGNAS, Lars Christer
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN

Doane, 10

Swecker & Mathis

LINDGREN, Per-Eric HOOK, Magnus

LINDBERG, Kjell Martin

NUMBER OF SEQUENCES:

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US-09-556-877-136/c
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                                                                                                                                                                                                           Sequence 136, Application US/09556877 Patent No. 6432916
                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                               GENERAL INFORMATION:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
                                                                                                                                                             APPLICANT:
                                                                                                                                                                           APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1374 base pairs
TYPE: nucleic acid
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FILING DATE: 25-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reb, Teresa Stanek
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                                                                                                                                                                                                                                                                                                                 262 CTGAAGGTTCTGACGGTATCAGTG
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REFERENCE/DOCKET NUMBER: 012885-074
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PRY: United States
22313-1404
                                                                                                                     Bhatia, Ajay
Skeiky, Yasir
Fling, Steve
                                                                                                      Maisonneuve, Jeff
                                                                                                                                                                           Probst, Peter
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P.O. Box 1404
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836-2021

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Pred. No. 12;
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US-09-620-412C-136/c
Sequence 136, Application US/09620412C
Patent No. 6448234
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US-09-370-807-7
                                                                                                                   ; ORGANISM: Oryza sativa
US-09-370-807-7
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; SEQ ID NO 136
rengTH: 882
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SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 136
LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
                                                                 Query Match
Best Local (
                                                                                                                                                                                     SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09370807 Patent No. 6297034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.3
Best Local Similarity 76.9
Matches 30; Conservative
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                                                                                                                                                                                                                                                                  APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/096,225
EARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE:
                                                                                                                                                                                                    SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Chlamydia
                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Chlamydia
                                                                                                                                                                   LENGTH: 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 GATCTTTCACCTTGGAGCATGTTTCTTCTTCTTTGCCGG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 GATCTTTCACCTTGGAGCATGTTTCTTCTTTTTTTTGCCGG 329
30 TTTTTCATCTTTGCAGGGACTTCTGGGGCCCGAGTATGTAAAACTCCTGGGTCTCTGTGT 89
                                                   Local Similarity
mes 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTTGCAGG 46
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                                                   Conservative
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57.0%;
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Pred. No. 17;
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Pred. No. 1;
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Pred. No. 1:
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Listing first 45 summaries
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              Published_Applications_Na:*

1: /cgn2_6/ptodata/1/pubpna/rg
2: /cgn2_6/ptodata/1/pubpna/rg
3: /cgn2_6/ptodata/1/pubpna/rg
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: /cgn2_6/ptodata/1/pubpna/VGSOB_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 270, App	1667	Seguence 1666 An	Sequence 1665, Ap	Sequence 1667, Ap	Sequence 1666, Ap	Sequence 1665, Ap	Sequence 1450, Ap	Sequence 118, App	Sequence 118, App	Sequence 609, App	Sequence 609, App			Sequence 14866, A	Sequence 31393, A	Sequence 8153, Ap	Sequence 1, Appli	Sequence 9118, Ap		Description	

21 26.4 23.8 385 10 US-09-770-791-90-
23.8 170834 100 23.8 170834 100 23.6 26225 100 23.4 4235 100 23.4 1548 100 23.4 1548 100 23.4 15620 100 23.4 5709 9 23.4 5709 9 23.1 440 9 23.2 1659 100 23.1 144 100 23.1 144 100 23.1 144 100 23.1 1516 100 23.1 32169 100
1656 1656 170834 170834 10 26225 10 26225 10 432 11548 10 1548 10 1549 10 1640 10 1440 10 1440 10 1184 10 10 1184 10 10 1184 10 10 1184 10 10 1184 10 10 1184 10 10 1184 10 10 1184 10 10 10 1184 10 10 10 10 10 10 10 10 10 10
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ALIGNMENTS

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PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR APPLICATION NUMBER: PCT/US01/00662 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00661 PRIOR FILING DATE: 2001-01-30	APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION APPLICATION	APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION APPLICATION FILING DATE:	CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03 PRIOR APPLICATION NUMBER: US 05/236,359 PRIOR APPLICATION NUMBER: US 60/236,359	SINGLE EXON NUCLEIC
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Patent No. US20020150891A1
GENERAL INFORMATION:
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SOFTMARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 9118
LENGTH: 570
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN EFFAL LIVER, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
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TELEFAX: (
                    REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAY.
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                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTINUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rowen, Lee APPLICANT: Koop, Ben F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Co
CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 GAATGGATCTCCTGCCTTGCGGGATTCCTTGGGCTGGAGTATGTAAAATTCCTGGGTCT 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GGATTCTTTTCATCTTTGCAGGGACTTCTGGGGCCGGAGTATGTAAAACTCCTGGGTCT 83
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 69; Conserv
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                                                                                                                                                                                                                                                                                                                                             98104-7092
                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                        E: Seed and Berry 6300 Columbia Cent
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                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hood, Leroy E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                682-6031
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79.38;
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Pred. No. 1.2e-10;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                            701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEF

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: ACCOLAGE V. 1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: WS 60/207,456

PRIOR APPLICATION NUMBER: WS 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-918-995-8153
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FBSESEQ for Windows Version 3.0
SEQ ID NO 8153
TLENGTH: 428
TYPES: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8153, Application US/09918995 publication No. US20030073623A1
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Best Local Similarity
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LENGTH: 684973 base pairs
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78.4%;
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71.98;
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Pred. No. 8.2e-09;
0; Mismatches 27;
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FILING DATE: 2000-09-27

APPLICATION NUMBER:

FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-10

2000-10-04 2000-08-03

GB 24263.6 60/236,359

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RESULT 5
US-09-864-761-14866
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                                                                                                                                                                                                            Sequence 14866, Application US/09864761 Patent No. US20020048763A1
                                                                                                       APPLICANT:
APPLICANT:
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                   APPLICANT: Penn, Sharron G.
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OTHER INFORMATION: EXPRESSED IN FETEL LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6

OTHER INFORMATION: SWISSPROT HIT: P98161, EVALUE 3.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AI792950.1, EVALUE 6.00e-07

OTHER INFORMATION: NT HIT: AL163210.2, EVALUE 4.00e-04
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                GTGGCTGCTCTACT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                          GCAGATGCTCTGCT
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                                                                                                                                                 Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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70.3%;
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Pred. No. 0.00043;
0; Mismatches 22
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US-09-954-456-922/c
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                                                                                                                                                                                              RESULT
                                                                                                                                       Sequence 922, Application Patent No. US20020115057A1
                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                            Best
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TITLE OF INVENTION: Process for Identifyin TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76 CURRENT APPLICATION NUMBER: US/09/954,456 CURRENT FILING DATE: 2001-09-18 PRIOR APPLICATION NUMBER: US/60/233,617
                                                                                                          APPLICANT: Young, Paul
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OTHER INFORMATION:
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OTHER INFORMATION:
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 2000-0
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Pred. No. 0.0006;
Pred. No. 22;
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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NUMBER OF
SOFTWARE:
                                        PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
                                                                                                                                             PRIOR FILING DATE: 2000-09
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/60/235,711
                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/60/235,637 PRIOR FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/60/235,134 PRIOR FILING DATE: 2000-09-25
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NOFTWARE: PatentIn ver
JQ ID NO 922
LENGTH: 369
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PRIOR APPLICATION NUMBER: US/60/235,720
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                                                                                                     PRIOR APPLICATION NUMBER: US/60/235,840
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ORGANISM: Homo sapiens
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                  SEQ ID NOS:
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Pred. No. 1
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; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo s
US-09-954-456-1538
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US-09-764-870-609
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US-10-125-540-609
                                                                           US-09-764-870-609
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LENGTH: 1314
TYPE: DNA
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Best Local Similarity
Matches 52; Conserv
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LENGTH: 369
Query Match
Best Local Similarity
Matches 55; Conserv
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LENGTH: 1314
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CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,870 CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                     Prior application data removed - NUMBER OF SEQ ID NOS: 646
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: \mbox{\rm PTZ}14
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                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
                                                                                                                                                                   SOFTWARE: PatentIn Ver.
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                                                                                                             TYPE: DNA
                                                                                            ORGANISM: HOMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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US-10-125-540-118
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US-09-764-870-118
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                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/09764870 Patent No. US20020042386A1 GENERAL INFORMATION:
                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 342
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                CURRENT FILING DATE: 2001-01-17
Prior application data removed -
NUMBER OF SEQ ID NOS: 646
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/764,870 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PTZ14
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                             NAME/KEY: SITE LOCATION: (134)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (134)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
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                                                                                                     ORGANISM: Homo sapiens
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LOCATION: (286)
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                                                                                                                            TYPE: DNA
OCATION: (286)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGGTGGATCTTTTGCCTTGCAGGATTCTTTTTCATCTTTGCAGGGACTTCTGGGGCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAATACAAAACCCCTGGGACACTGCCTGGCCCATAGTG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 25.2%;
l Similarity 55.0%;
55; Conservative
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Pred. No.

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1450
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILLING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 08/420,856 PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dillon, Patrick J
APPLICANT: Haseltine, Willia
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
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                                                                                                           OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (274)
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                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (266)
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NAME/KEY: misc feature
LOCATION: (265)
OTHER INFORMATION: n equals a,t,g,
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                                                         OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (275)
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NAME/KEY: misc feature
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Pred. No. 2
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or

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Sequence 165, Application US/10092154

Publication No. US20030054375A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC009C1

CURRENT APPLICATION NUMBER: US/10/092,154

CURRENT FILING DATE: 2002-03-07

NUMBER OF 520 ID NOS: 2003

PUTOR Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1665

LENGTH: 504
                                                                                                 RESULT 14
US-10-092-154-1666/c
: Sequence 1666, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
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Best Local Similarity
Souther 50; Conserve
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LOCATION: (399)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (402)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (403)
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC009C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
-10-092-154-1665
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OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                            66 TGTAAAACTCCTGGGTCTCTGTGTGTGC 93
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56.8%;
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67.3%;
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Pred. No. 6.
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Pred. No. 3;
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                                                                       Antibodies
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RESULT 15
US-10-092-154-1567/c
US-10-092-154-1567/c
; Sequence 1667, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
Search completed: April 25, Job time : 228 secs
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1666
                                                                                                                                                                                                                                                                                                       ; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1667
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 50; Conserv
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1666
LENGTH: 504
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Best Local
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEO ID NOS: 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
FILE REFERENCE: TO TO THE T
                                                                           261 AGGAACTATGCTAGGTCCCAGTGTGTGC 234
                                                                                                                                                     321 TTGGTTGTTTGTCCTTCAGTCCTCCTTTTCTTAAACACAGAGCCAGCTCCTGGCATAGGC 262
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                                                                                                              66 TGTAAAACTCCTGGGTCTCTGTGTGTGC 93
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Pred. No. 6.1;
0; Mismatches
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Pred. No. 6.1;
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